

FIG. 1A

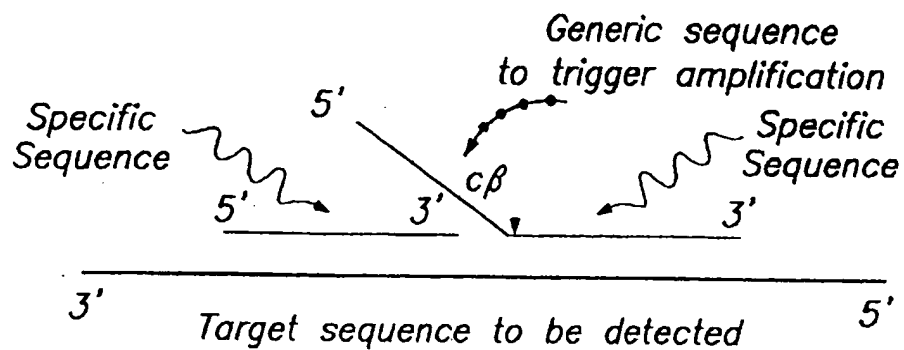


FIG. 1B PART ONE: TRIGGER REACTION

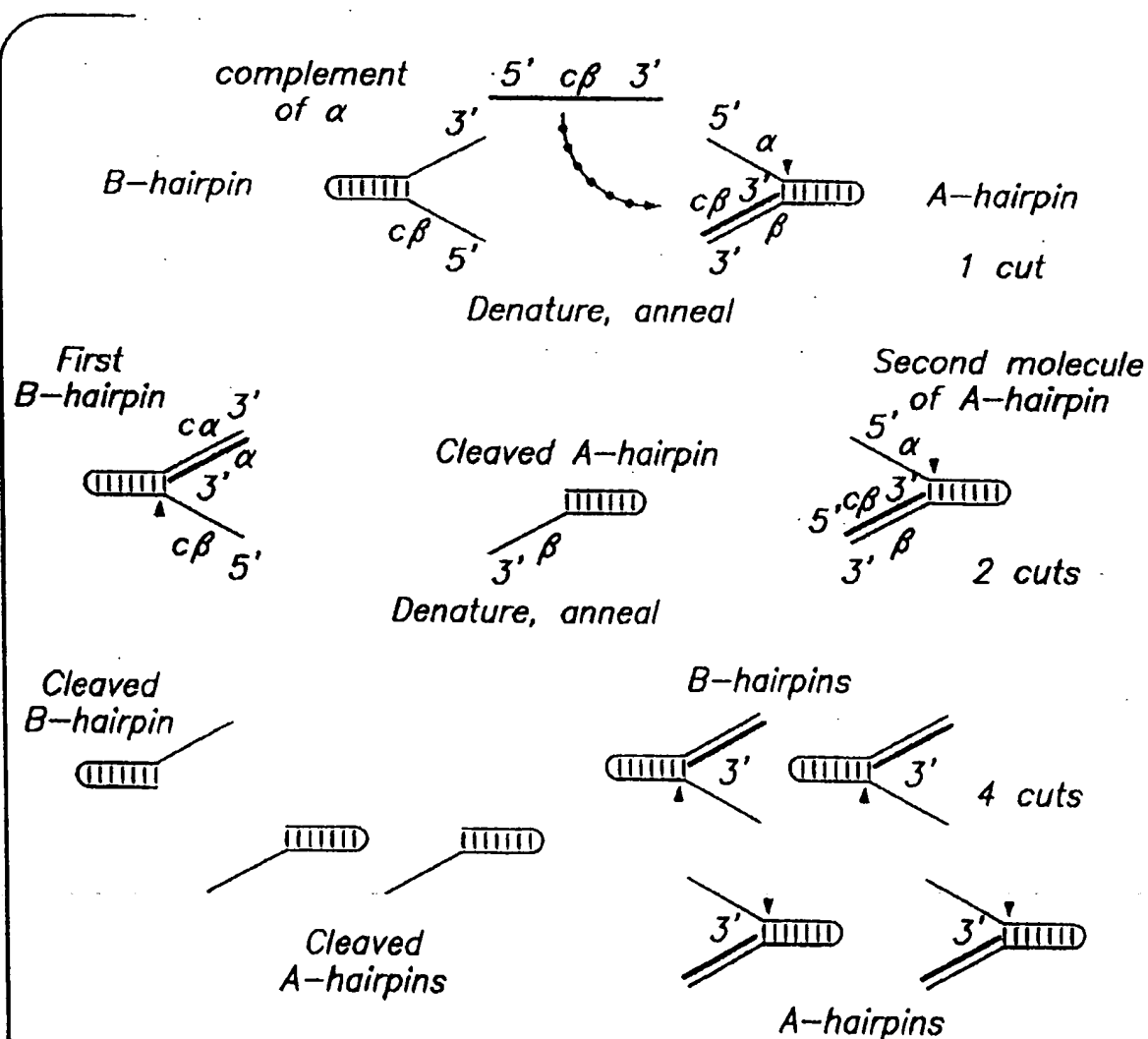


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

[illegible]

FIG. 2B

[illegible]

FIG. 2C

MAJORITY [SEQ ID NO:73]	TCCAGGCCCCACATCGAXGACCTGAXGCTCTCCTGGAGGCTXTCCGAGGTGCCGACCGACCTGCCCCCTGGA	
DNAPTAQ [SEQ ID NO:1]C..T...A.....C..GG..A.....	764
DNAPTFL [SEQ ID NO:2]GGG.....G.C...GCC.T...C..A...T...A...T.....	761
DNAPTTH [SEQ ID NO:3]	..A.....C...A...C.G.....T.....C...G.....C.....	770
MAJORITY	GGTGGACTTGGCCGAGXGGGGGAGGGCGGACCGGAGGGGCTTAGGGCCCTTCTGGAGAGGCTGGAGTTT	
DNAPTAQAA.....A.....A.....T.....T.....T.....	834
DNAPTFLGG.G.C.C.C.CACA...A...T.....T...GG...T...T.....C..T.....	831
DNAPTTHC.....C..G.....A.....A.....C.....G.....C.....	840
MAJORITY	GGGAGCCCTCCTCGACGAGTTCGGCCCTCCTGGAGGGCGCCGAGGGCCCTGGAGGAGGGCCCTGGCCCGCGG	
DNAPTAQT.....AA.....	904
DNAPTFL	..A.....G.....G..G...GGCA.....	901
DNAPTTHC.....C...GGC.....	910
MAJORITY	CGGAGGGGCGCTTCGTGGGCTTGTGCTTTCGGGGCGGAGGCGGATGTGGGGCGGAGCTTCTGGCCCTGGC	
DNAPTAQT.....G.....AAG.....T.....	974
DNAPTFLT..TT.....TC.T.....T.....	971
DNAPTTHC.....C.....G.....AAA.....	980
MAJORITY	CGCCGCCAGGGAGGGCGGGGTCCACCGGGGACGACACCCCTTTAXGGGGCTTAXGGGACCTXAAGGAGGCTG	
DNAPTAQG.....C..C..G..T.A..AA.G...G.....C.....	1044
DNAPTFL	T.GG..GT.....G..CC...T.....A.....C...G...G.....T.....G.....	1041
DNAPTTHTG.....C.....G.....GGC...G..A.A.....C.....C 1050	

MAJORITY [SEQ ID NO:7] CGGGGXCTCCTGGCCAGGACCTGGCCGTTTTGGCCCTGAGGAGGGCCTCXTGCCCGGGGACG

DNAPTAQ	[SEQ ID NO:1]	G.	T.	A.		AG.	C.		A.		T.	G.	CG.		6.	1114	
DNAPTFL	[SEQ ID NO:2]	AA.		G.		G.			C.			6.		T.	C.	A.	1111
DNAPTTH	[SEQ ID NO:3]		C.			G.		C.		TC.		G.	A.		6.		1120

MAJORITY ACCCGATGGTCCTCGGGTACCTCCTGGACCCCTCGAACACCGACGCCCGAGGGGCTGGCCCGGGGCTACGG

DNAPTAQ	T	1184
DNAPTFL	T	1181
DNAPTTR	G	1190

MAJORITY EGGGGAGTGGACGGAGGAXCGGGGGGAGCGGGGGCTCTXTGGAGAGGGCTCTTGGXGAACCTXXXGGAG

C.	G.	GC.	T.	CCC.	GTG..	G.
DNAPTAQ	T.	A.	GG.	A.	C.	AAA..
DNAPTFL	G.	CCC.C.	C.G.	CAT.G.	CCCTA..	
DNAPITH						

MAJORITY CCGCTGAGGGGGAGAGAGGCTCCTTG9CTTACCAAGAGGTGGAAGA8CCCCCTTCCC6GGTCCTCGG

[illegible]

MAJORITY CCGACATGGAGGGGACGGGGGTXCGGCTGGAGGTGGCTACCTCCAGGGCGTCTCCCTGGAGGTGGCGCA

DNAPTAQ	G. C.	T. AG.	T. G.	C.	1394
DNAPTFL	GG	C.	C.	A. C	1391
DNAPTHH	C.	A.	T.	C. T.	1400

FIG. 2E

MAJORITY [SEQ ID NO: 7]	GGAGATCGGCGCGCTCGAGGAGGAGGCTTCCGCCCTGGCGGGCCACCCCTTCAAGCTCAAGTGGCGGGGAC	1464
DNAPTAQ [SEQ ID NO: 1]GC.....CG.....	1461
DNAPTFL [SEQ ID NO: 2]	...G.G...AG.G.....	1470
DNAPTTH [SEQ ID NO: 3]T.....G.....	
MAJORITY	CAGCTGGAAAGGGTGCTCTTTGACGAGCTXGGGCTTCCGGCCATCGGCAAGACGGGAGAGACXGGCAAGC	
DNAPTAQG.....A.....	1534
DNAPTFLGC.....G.C.G.T.....	1531
DNAPTTHTA.....T.G.G.....C.A.....	1540
MAJORITY	GCTCCAGCAGCGCGCGCTGCTGGAGGGCCCTXCGXGAGGGCCACCCCATCGTGGAGAGATCCTGCCAGTA	
DNAPTAQG.....C.....	1604
DNAPTFLT.....G.A.....CGG.....	1601
DNAPTTHG.....A.G.....	1610
MAJORITY	CGGGGAGGCTCAGCAAGCTCAAGAACACCTAGATXGACCCCGCTGCCXGXCTGGTCCAGCCCGAGGAGCGGGC	
DNAPTAQG.....T.....G.A.....	1674
DNAPTFLA.....C.C..G.....A..C..	1671
DNAPTTHG.G.....C.AAG.....G.....	1680
MAJORITY	GGCGTCCACACCCCGCTTCAACGACAGACGGGCCACGGGCCAGGGCTTAGTAGCTCGGACCCCAACCTGC	
DNAPTAQA.....T.....C..	1744
DNAPTFLC.....TCC.....	1741
DNAPTTHG.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCGCCGCTCGGACGCCXCTGGGCGAGAGGATCGGCGCGGCGCTTCGTGGCCGAGGAGGGXTGGGT	
DNAPTAQ [SEQ ID NO:1]G..T..G.....A..C.....G...C..	1814
DNAPTFL [SEQ ID NO:2]G.....T.....C..C.....A.....C.....	1811
DNAPTTH [SEQ ID NO:3]CT.....C.....T.....C.....T.....C..	1820
MAJORITY	GTGGTGGGCTGGACTATAGCCAGATAGAGCTCGGGGTGCTGGCGCGACCTCTCCGGGGACGAGAACCTG	
DNAPTAQ	A.....T..T.....C.....A.....G.....C.....	1884
DNAPTFL	.C.....T..T.....C.....T.....T.....T.....	1881
DNAPTTHC.....C.....C.....C.....A.....	1890
MAJORITY	ATCGGGGTCTTCAGGAGGGGAGGACATCCACACCCAGACGGCGAGGTGGATGTTGGGGTCCCGCCCGG	
DNAPTAQG.....G.....G.....G.....G.....G..	1954
DNAPTFLT.....T.....T.....T.....T.....T..	1951
DNAPTTHA.....A.....A.....A.....A.....	1960
MAJORITY	AGCGCGTGGACCCCTGATCGCGCGGGCGGCCAAGACCATCAACTTCGGGGTCCCTCTACGGGCA1GTCCGG	
DNAPTAQA..G..A.....T.....G.....G.....G..	2024
DNAPTFLA..G..A.....T.....G.....G.....G..	2021
DNAPTTHA..G..A.....T.....G.....G.....G..	2030
MAJORITY	CCACCGGCTCTCGCAGGAGCTTGGCCATCCCGCTACGAGGAGGGGTTGGCCCTTCATTGAGCGGCTACTTCCAG	
DNAPTAQA.....A.....T.....CCA.....T.....	2094
DNAPTFLGG.....T.....T.....T.....T.....	2091
DNAPTTH	...TA..G.....T.....T.....T.....A.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:73]	AGCTTCCCAAGGTCCGGGCTGGATTGAGAGACCCCTGGAGGAGGGCCAGGGCGGGGTACGTTGGAGA	
DNAPTAQ [SEQ ID NO:12]	2164
DNAPTFL [SEQ ID NO:21]	A.....GG.....C.....C.CC.....T.....	2161
DNAPTTR [SEQ ID NO:31]A.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTGGGGGGGGGGGTACGTGCGCGAGCTCAAGGGCCGGGTGAAGAGGCTGCGGGGAGCGGGGGGA	
DNAPTAQC.....A.....AG.G.....C..	2234
DNAPTFLT.....C.....	2231
DNAPTTRAA.AA.....CA.....C.....	2240
MAJORITY	GGGCA TGCCCTTCAACA TGCCCGTCCAGGGCCAGCGCGCGGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQG.....T.....	2304
DNAPTFLC.....CG...T	2301
DNAPTTRC.....C.....	2310
MAJORITY	TTCCCGCGGCTXGAGGAAATGGGGCCAGGATGGTGGTXGAGGTCCAGGACGAGCTGGTCCCTCGAGGGCCC	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTRC.C.G...G.....C.C.....CC...G.....	2380
MAJORITY	CCAAAGAGCGGGGGAGCGGTGGCCGCTTGGCCCAAGAGGTCATGGAGGGGCTCTATCCCCCTGGCCCGT	
DNAPTAQ	A.....A.....CC.....CGGC.....G.....	2444
DNAPTFLG.C.....AG...A.....GG.....CAG..	2441
DNAPTTRC...C.....C...A.....G.....AA..C.....C.....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGTGGAGGTGGGGATGGGGAGGACTGGCTCTCCGCCAAGGACTAG	
DNAPTAO [SEQ ID NO:1]A.....	GA 2499
DNAPTFL [SEQ ID NO:2]CC.....	2496
DNAPTTH [SEQ ID NO:3]T.....	GT... 2505

FIG. 3A

MAJORITY [CSED ID NO:8]	MXAMLPIFEPKORVLLVDGHHLAYRTFFALKGLTTSRGEPUOAVYGFAXSLLKALKEDG-DAVXUVFDAQ	
TAD PRO [CSED ID NO:4]	RG.....H.....	69
TFL PRO [CSED ID NO:5]V.V.....	68
TTM PRO [CSED ID NO:6]	E.....YK.F.....	70
MAJORITY	APSRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPQYEADDDVLATLAKKAEKEGYEVAIL	
TAD PRO	GG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTM PROFT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSONLPGVKSIGEXTAXKLLX	
TAD PRO	K.....H.....D..A...T..E.....R...E	209
TFL PROE..I.....Y.....A.....I.....QR..IR	208
TTM PRO	V...V...H...E...F...V.....L...K	210
MAJORITY	EWGSLNLLKNLBRVKP-XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF	
TAD PRO	A.....L...AI...L...D..K..WD.AK.....K.....R.....	278
TFL PROFQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTM PROENV...K..L...R..LE..R.....L.OG.....	280
MAJORITY	GSLLHEFGLEXPKALEEAPWPPEGAFVGFVLSRPEPMHAEALLAALAAARXGRVHRAXDPLXGLRDLKEV	
TAD PROS.....K.....D.....G.....PE.YKA.....A	348
TFL PROG...A.....L..SF.....G.WE..L...Q...R.....G.	347
TTM PROA.AP.....K.....C.D.....A...A..K.....	350

FIG. 3B

MAJORITY [SEQ ID NO: 8]	RGLLAKOLAVLALREGDLXPCDDPHMLAYLLDPSNTTPEGUARRYGGEWTEGAGERALLSERLFXNLXX	
TAQ PRO [SEQ ID NO: 4]	S.....G. P.....E.....A.....A.....WG	418
TFL PRO [SEQ ID NO: 5]	I.....F. E.....A.....OT. KE	417
TTH PRO [SEQ ID NO: 6]	S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEIARLEEEVFRLAGHPFNLNSRD	
TAQ PRO	R...R...A.....R.....A.....A.....	488
TFL PRO	K.....E.....R.....EA.V.Q.....	487
TTH PRO	K.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PROS.....D. I.....	558
TFL PRODR.....A.....K..	557
TTH PRO	R...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNQTATGRLSSSDPNLQNI PVRTPLGQRI RAAFVAEEGWXLVALDYDOI ELRVLAHLSQDENL	
TAQ PROI.....L.....	628
TFL PROV..V.....	627
TTH PROA..A.....	630
MAJORITY	IRVFQEGROIHTQTASWMF GUPPEAVOPLMRRAAKTINFGVLYGMSAHLSDQLAI PYEEAVAFIERYFO	
TAQ PROE.....R.....Q.....	698
TFL PROS..G.....G..S.....	697
TTH PRO	K.....V.....	700

FIG. 3C

MAJORITY [SEQ ID NO:8]	SFPKVRAWI EKTLEEGRRRGYVETLFORRRYVPDLNARVKSUREAAERMAFNMPVOGTAADLMK LAMVKL	768
TAQ PRO [SEQ ID NO:4]E.....	767
TFL PRO [SEQ ID NO:5]	Y.....G.....R.	770
YTH PRO [SEQ ID NO:6]K.....	
MAJORITY	FPRLXEMGARM LQVHDELVL EAPKXRAEXVAA LAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX	
TAQ PROE.....E...A...R.....I.....	833
TFL PROO.L.....D...R.....W..O...L.....	831
YTH PROR.....L.....QA...E.....A..KA.....M.....G	835

Genes for Wild-Type and Pol(-)DNAPTaq

Domain
Coding Regions: 5' Nuclease

Polymerase

FIG. 4A

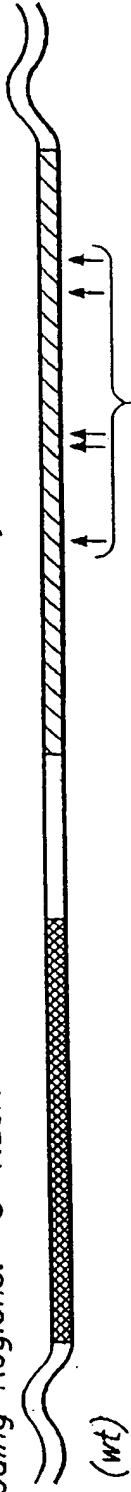


FIG. 4B

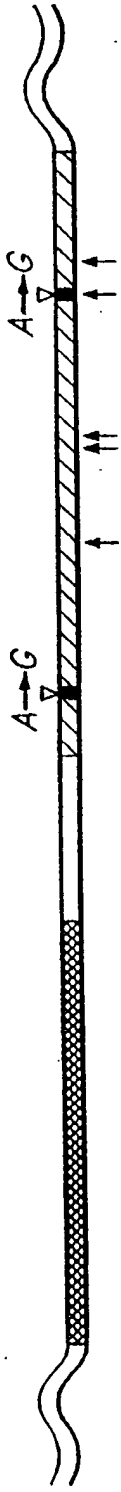


FIG. 4C



FIG. 4D

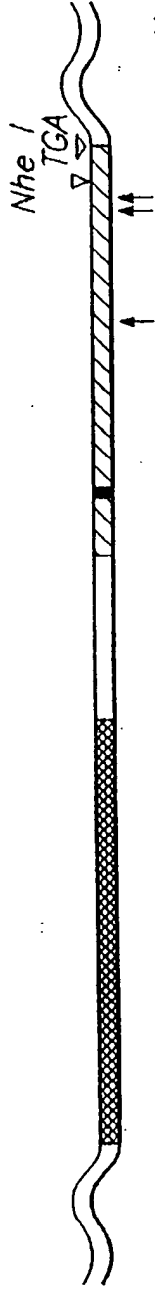


FIG. 4E



FIG. 4F

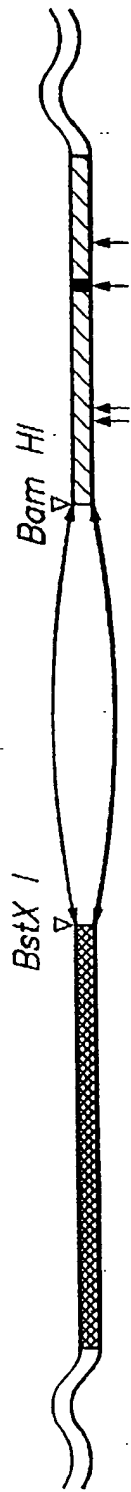
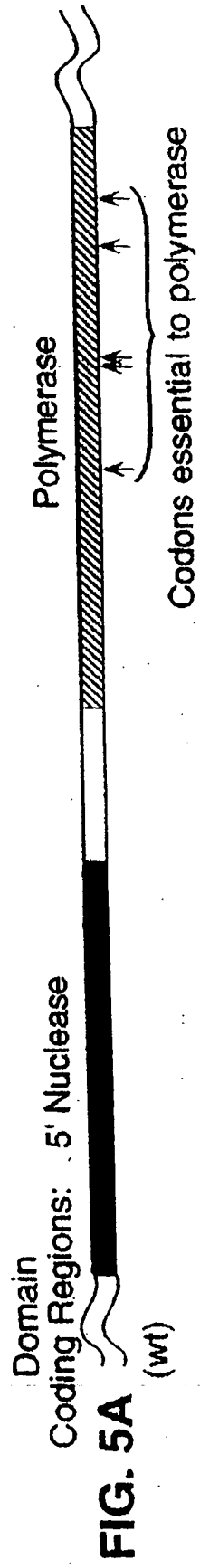


FIG. 4G



Genes for Wild-Type and Pol(-) DNAPTfl



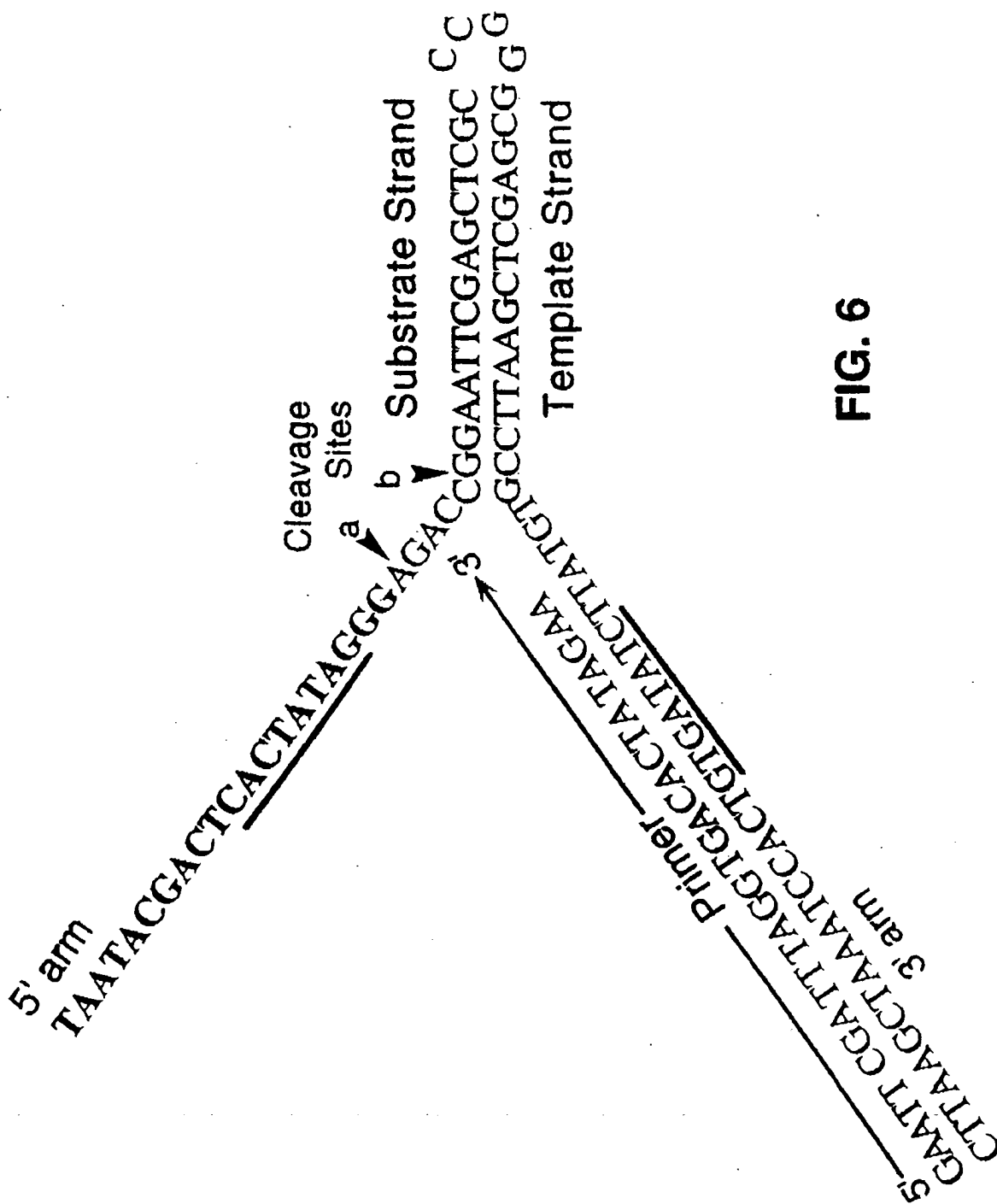


FIG. 6

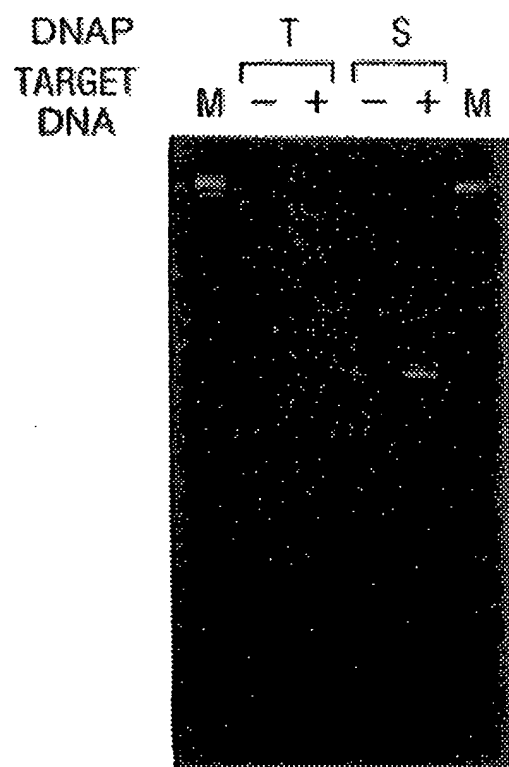


FIG. 7

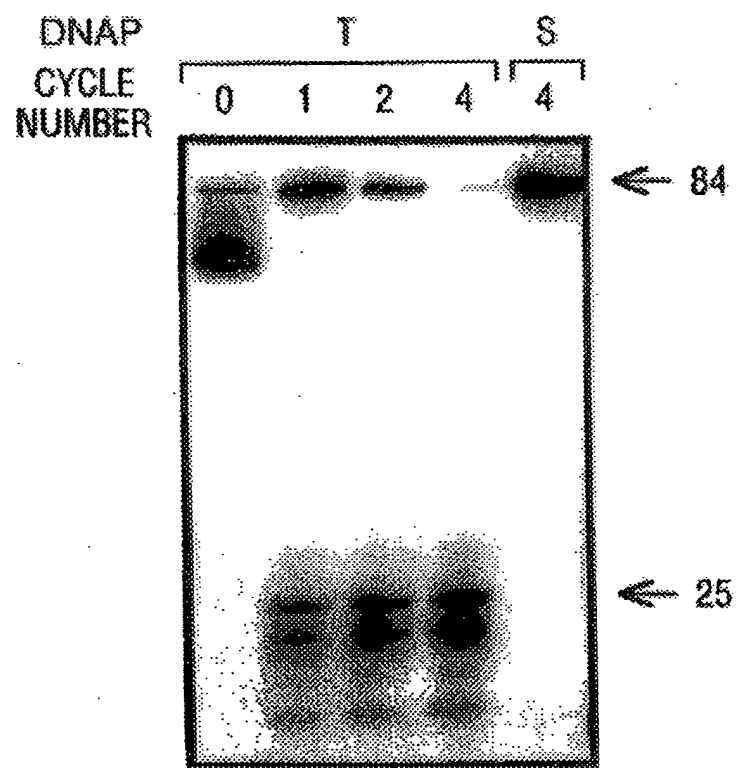


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

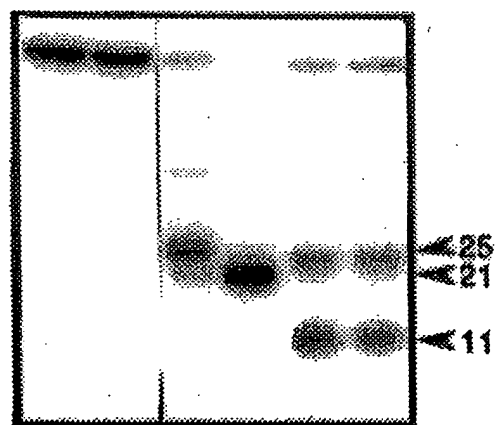


FIG. 9A



FIG. 9B

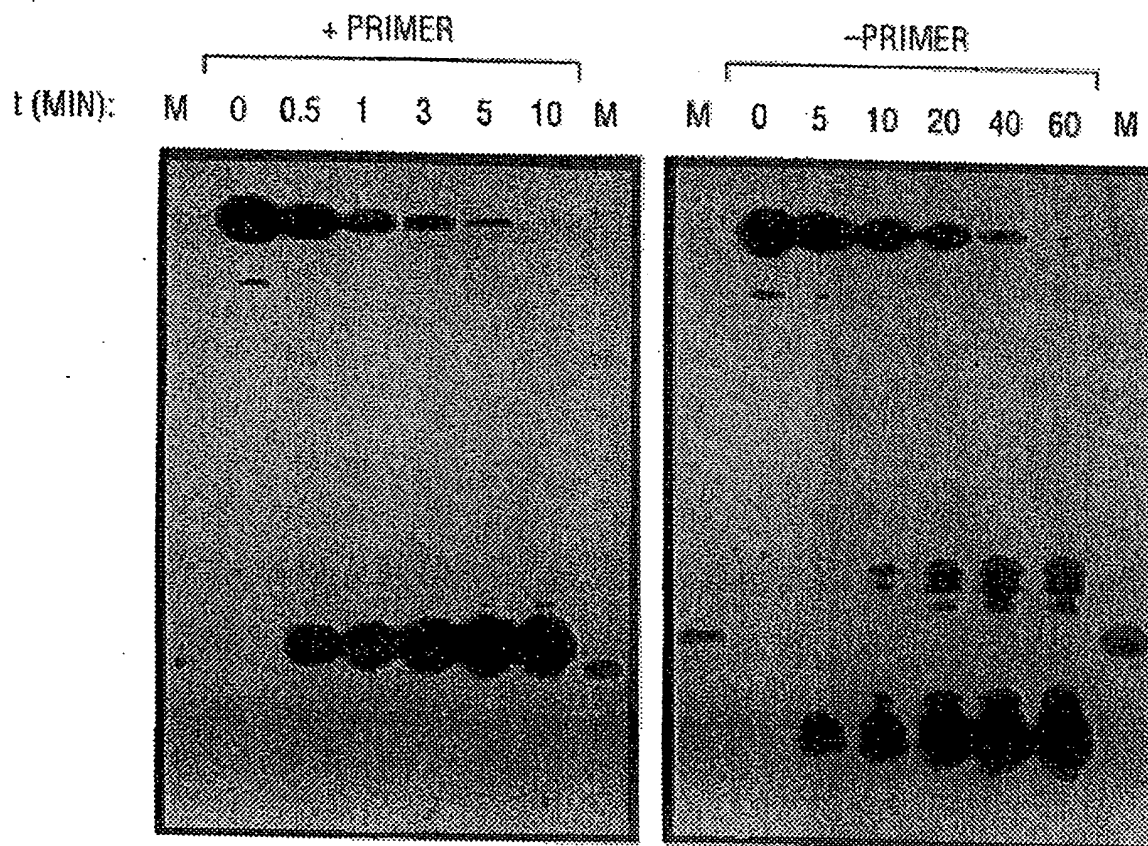
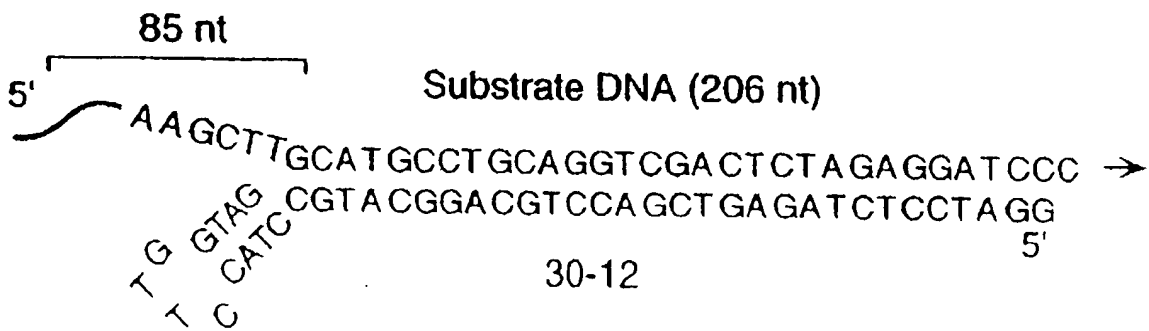
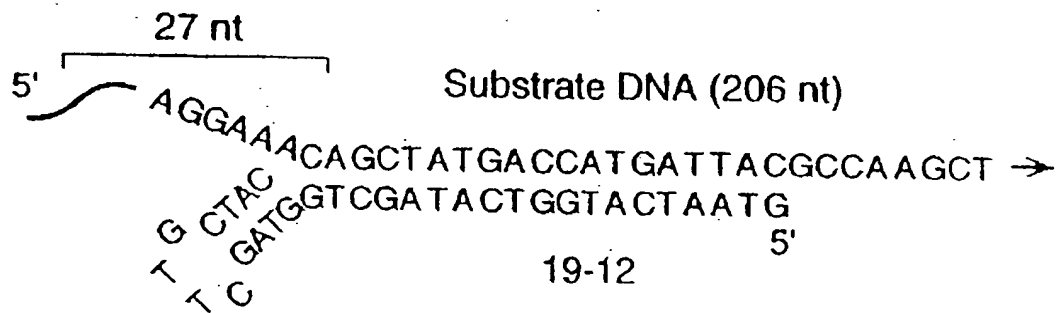


FIG. 10A

FIG. 10B

FIG. 12A



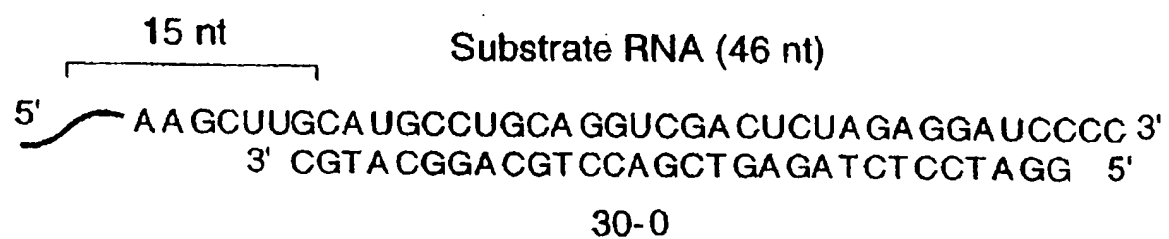


FIG. 13A

-35 -10 RBS
 TTGACAATTAATCATCGGCTCGTATAATGTTGTGGAATTGTGAGCGGATACAATTTACACAGGAACAGCG
 MetAsnSer...
 ATGAATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACTGGCC
 EcoRI KpnI BamHI Sall PstI SphI HindIII
 SstI XbaI

FIG. 14B

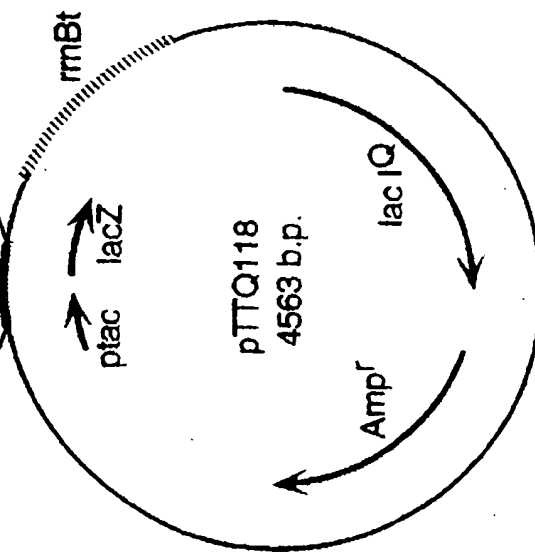


FIG. 14A

RBS: Ribosome binding site lacZ: Beta-galactosidase alpha fragment
 ptac: Synthetic tac promoter rmBt: E. coli rmB transcription terminator
 lac I^Q: Lac repressor gene

FIG. 14C

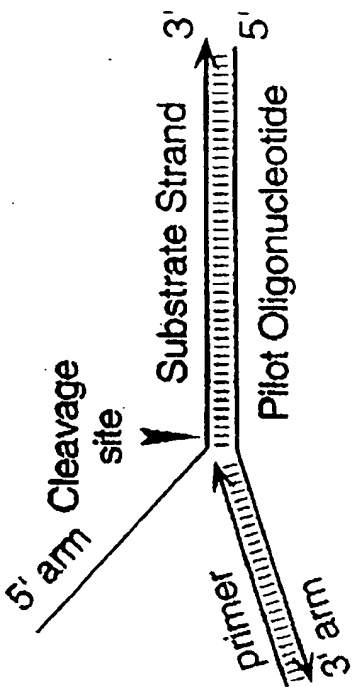


FIG. 16B

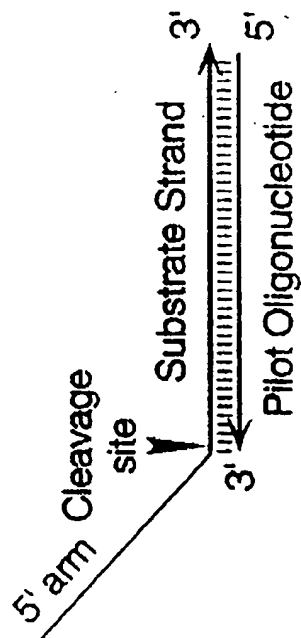


FIG. 16D

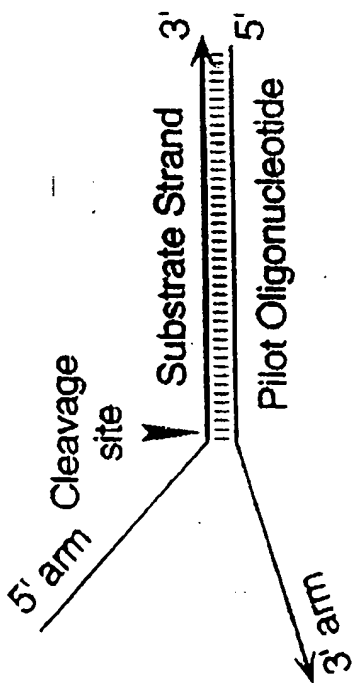


FIG. 16A

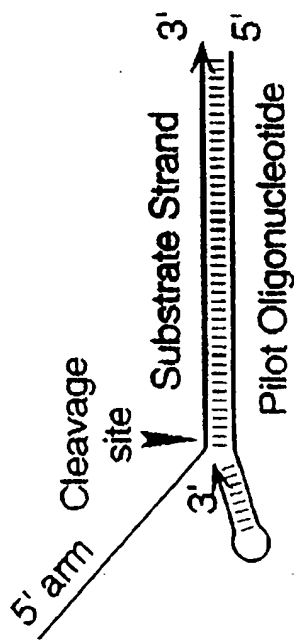


FIG. 16C

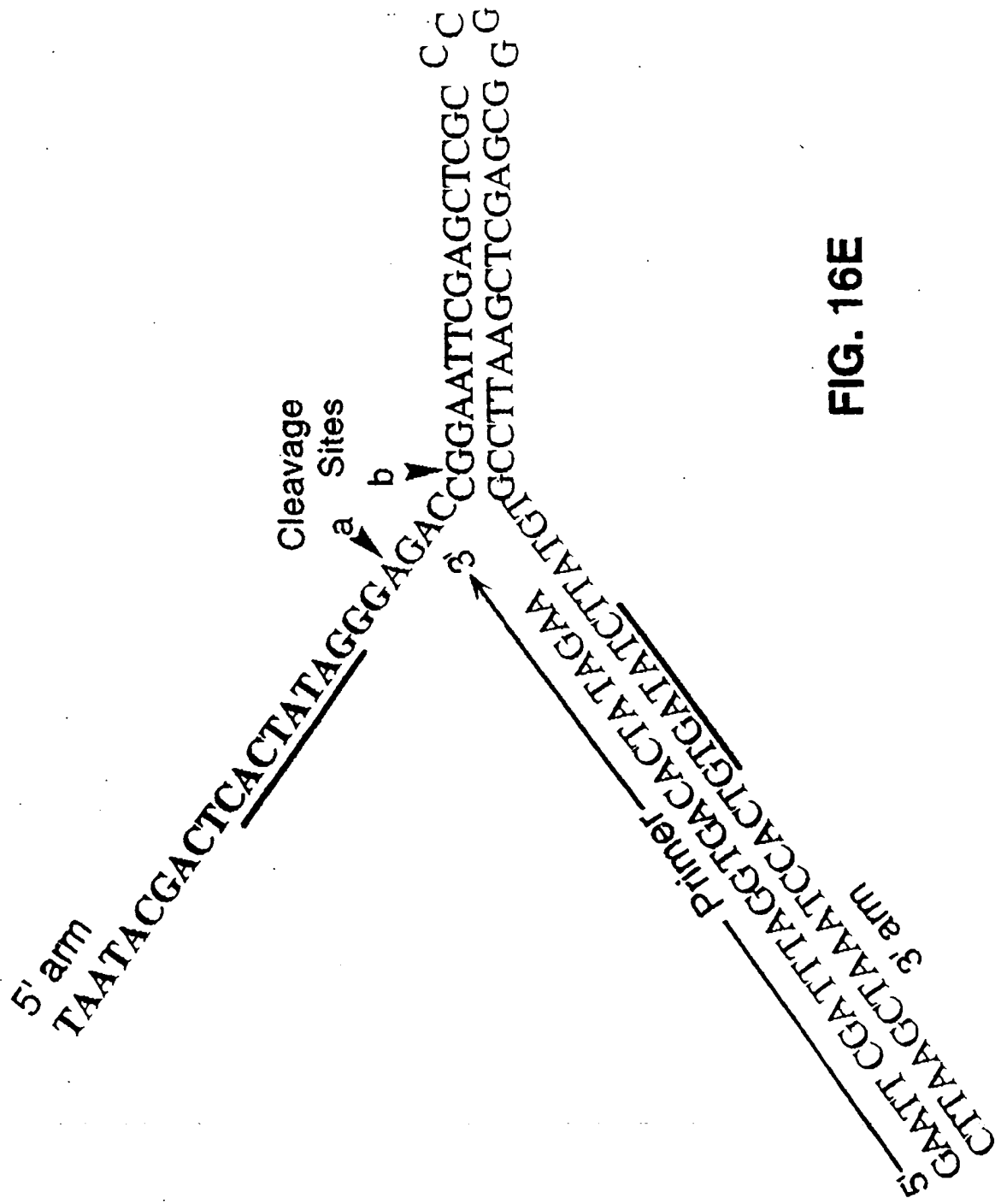
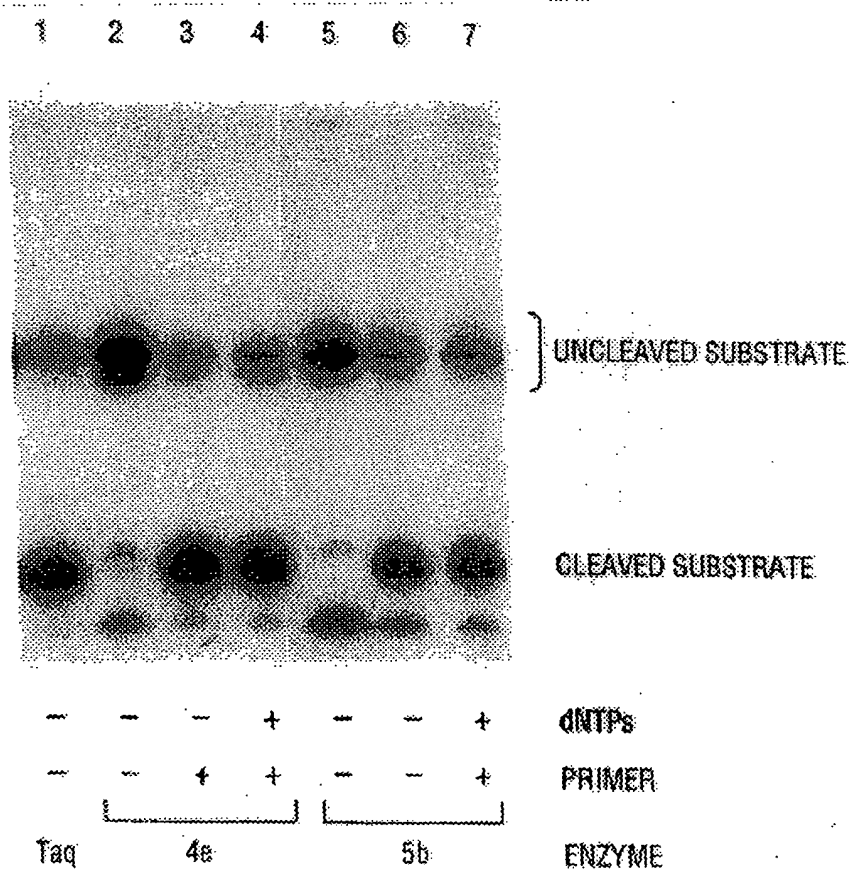


FIG. 16E

FIG. 17



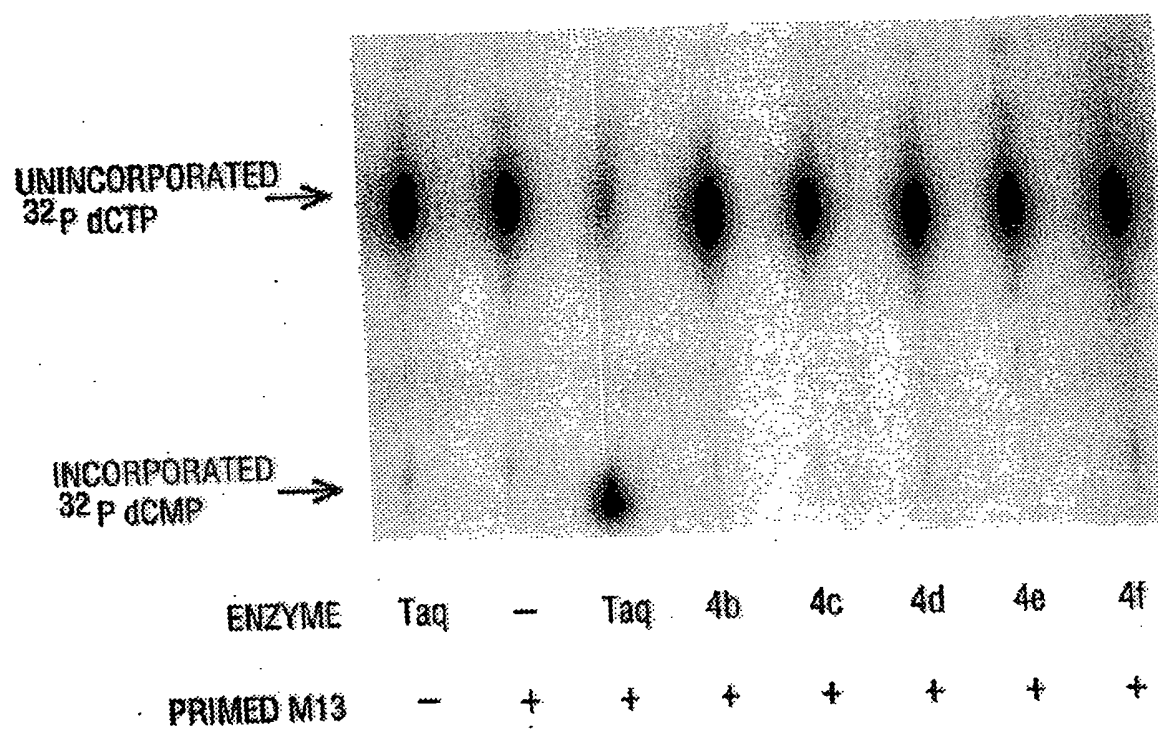


FIG. 18

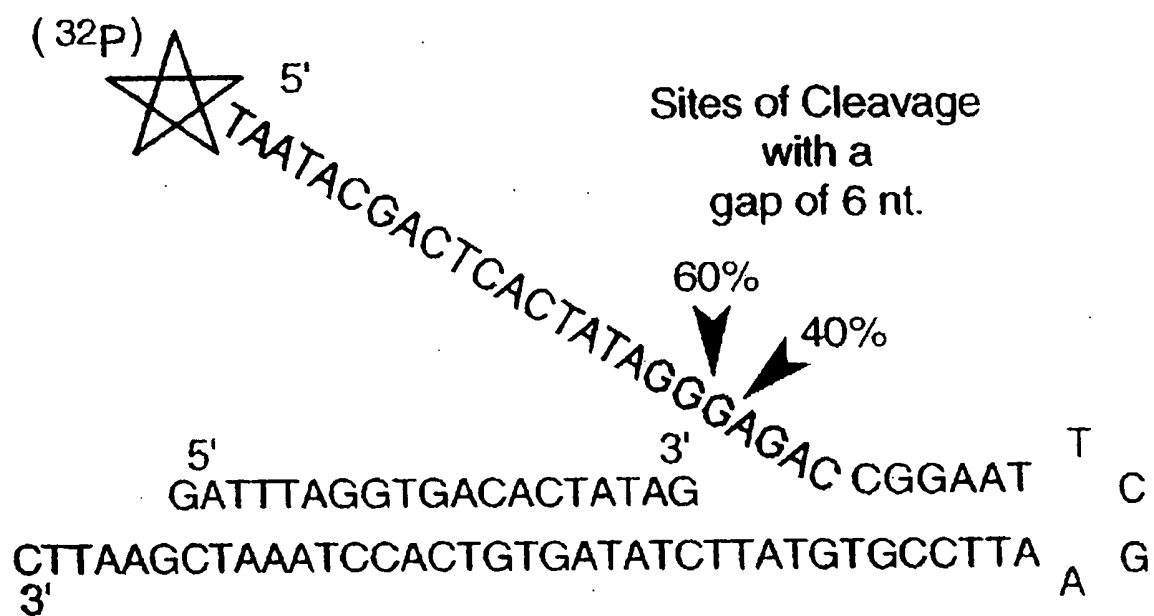


FIG. 19A

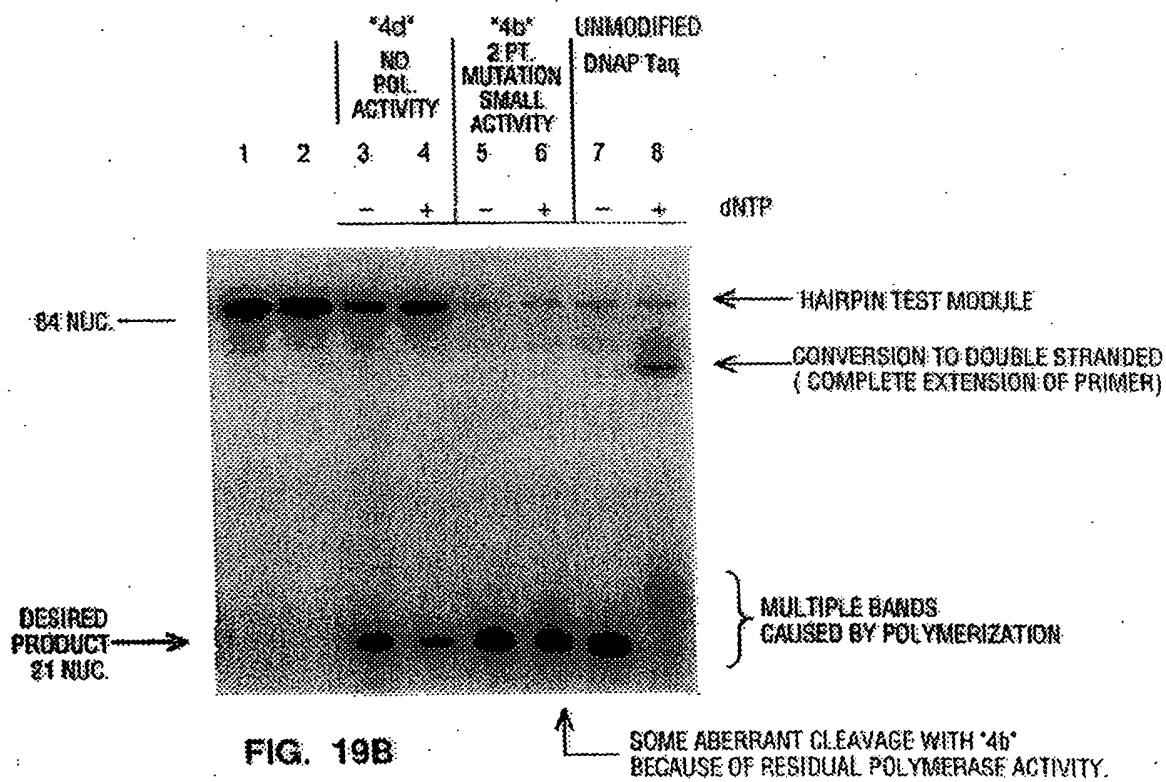


FIG. 19B

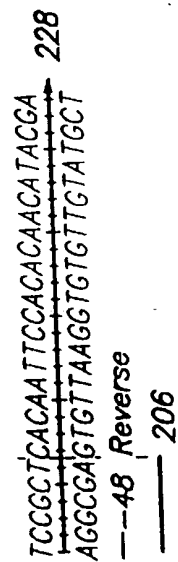
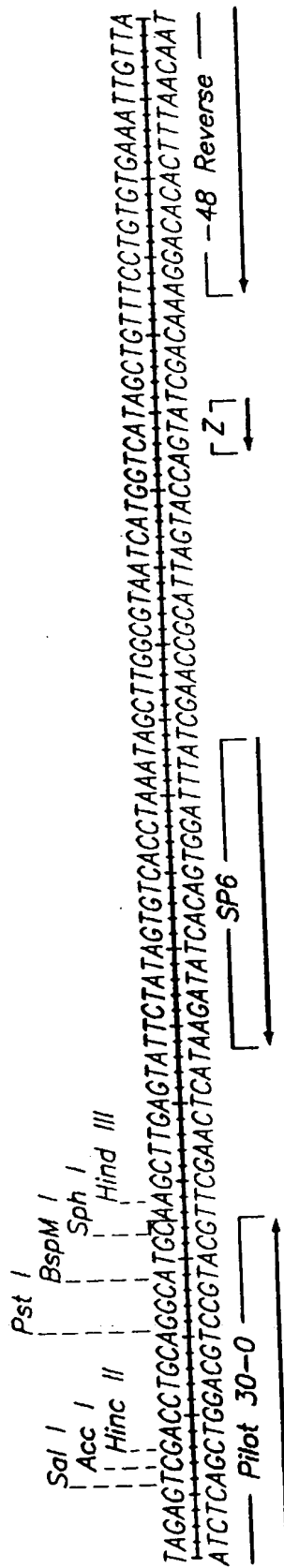
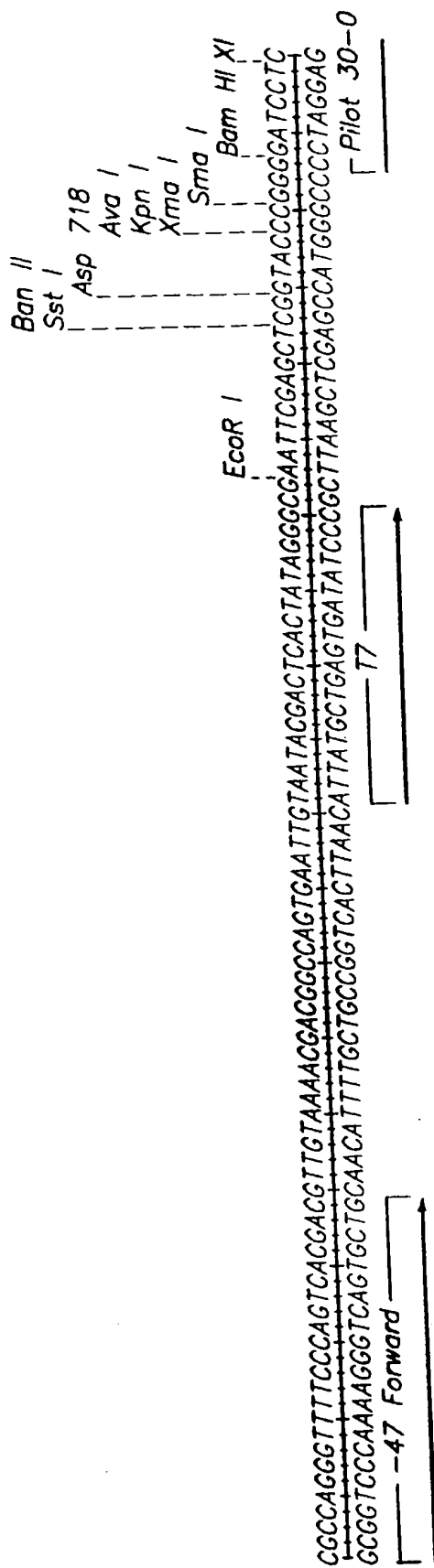


FIG. 21

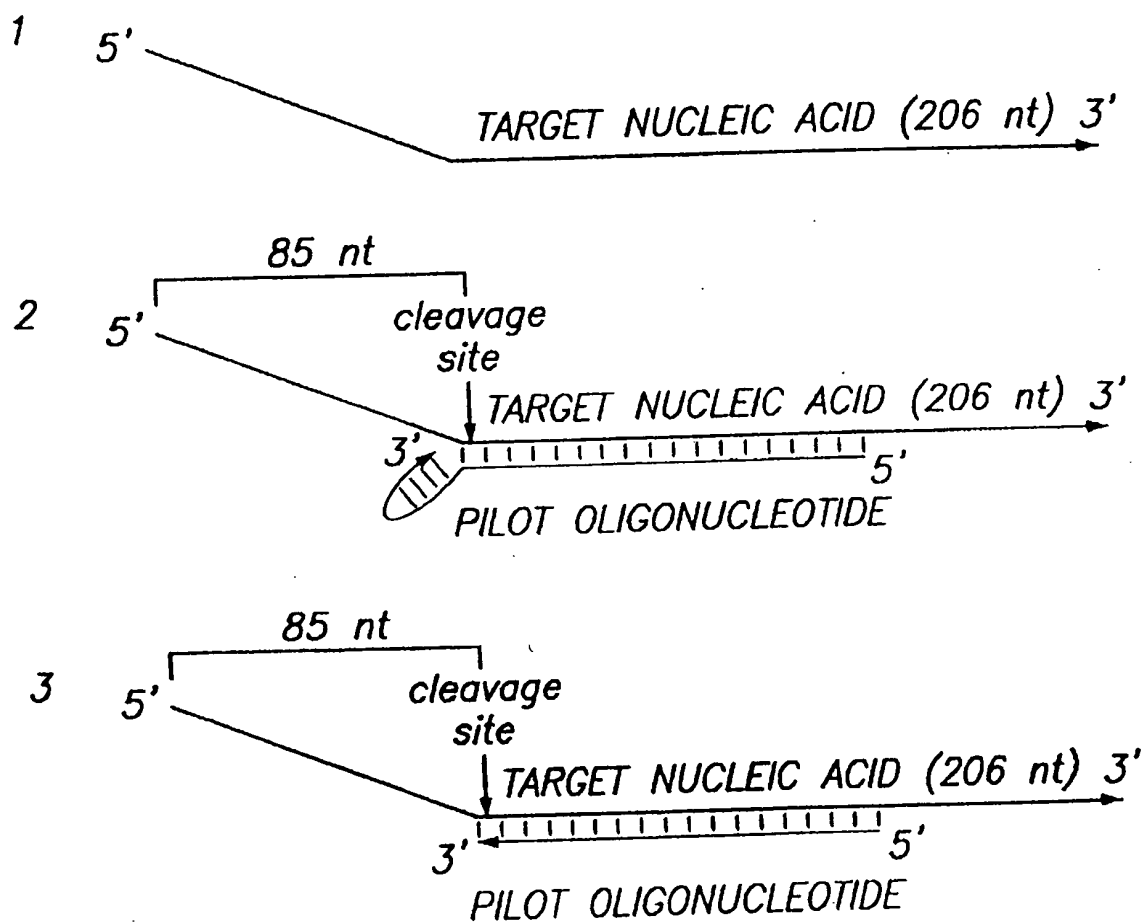


FIG. 22A

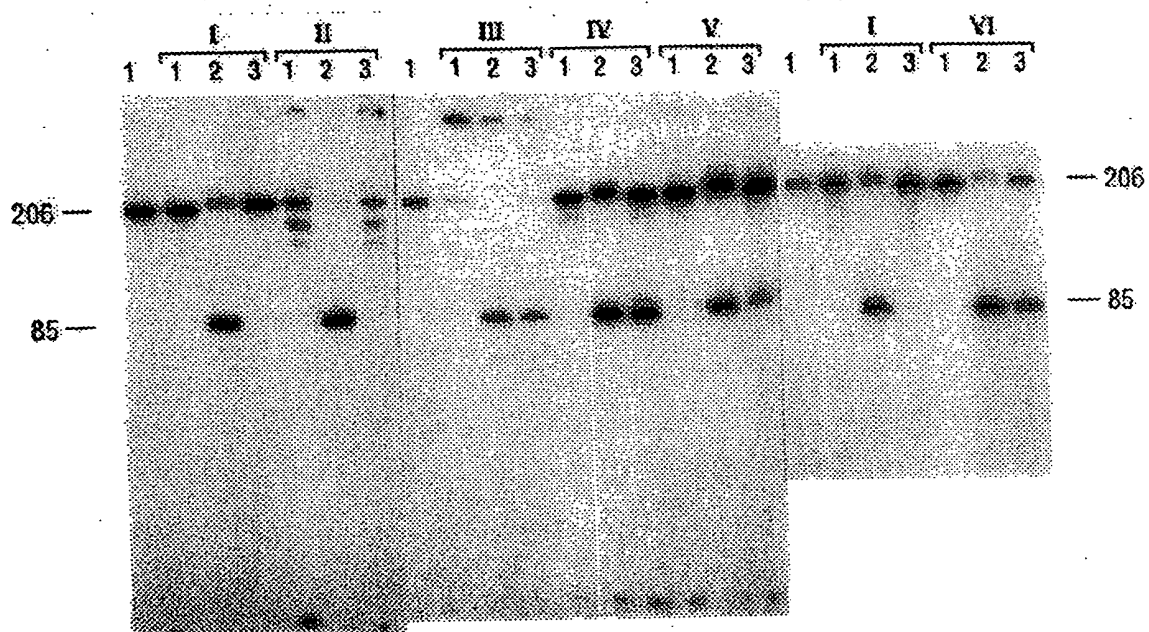


FIG. 22B

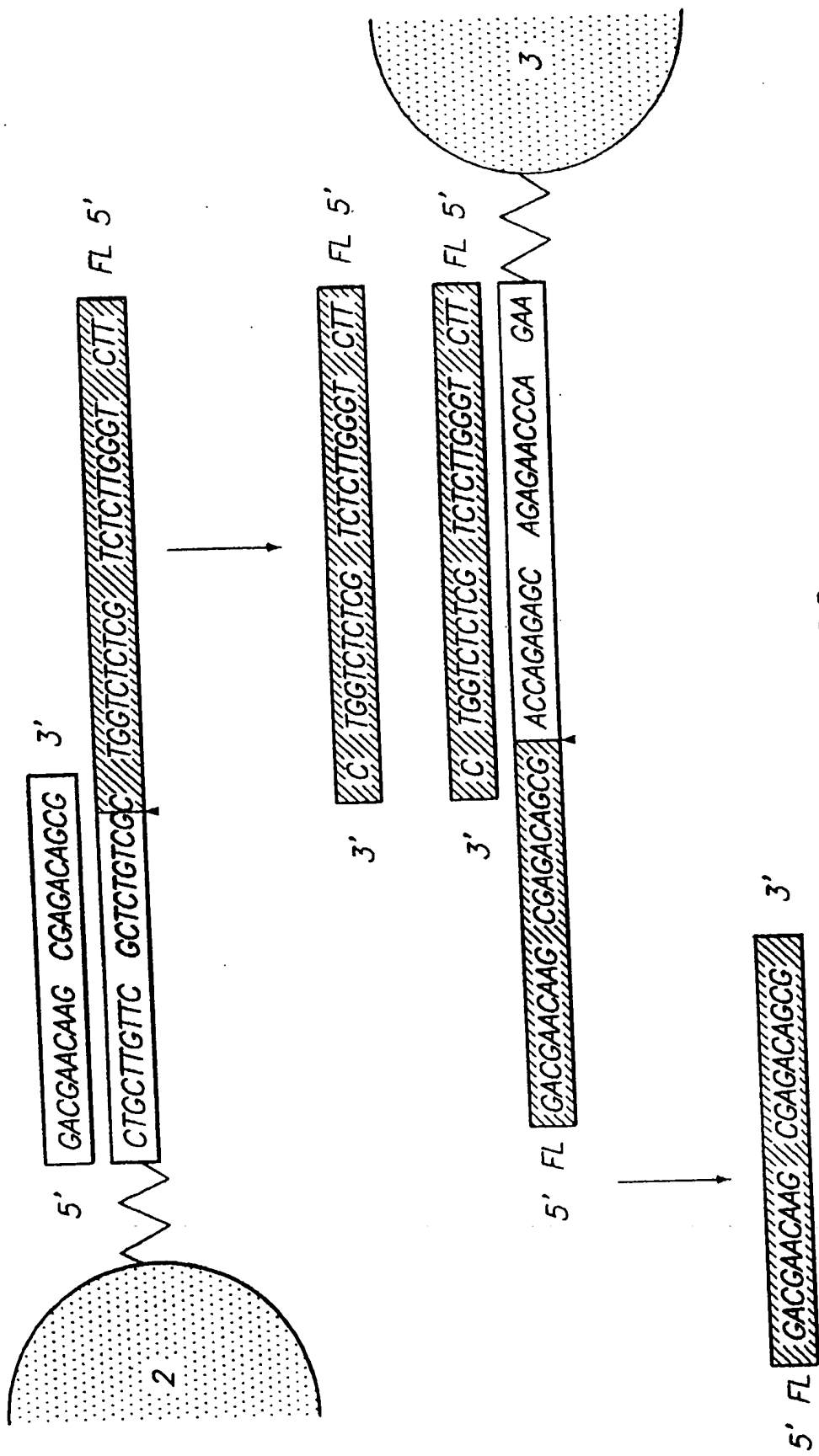


FIG. 23

CDR BEAD		T	T	T	AT	AT	A	A	A	
PILOT		-	-	+	-	+	+	-	-	
CLEAVASE	M	M	-	+	+	+	+	+	-	M

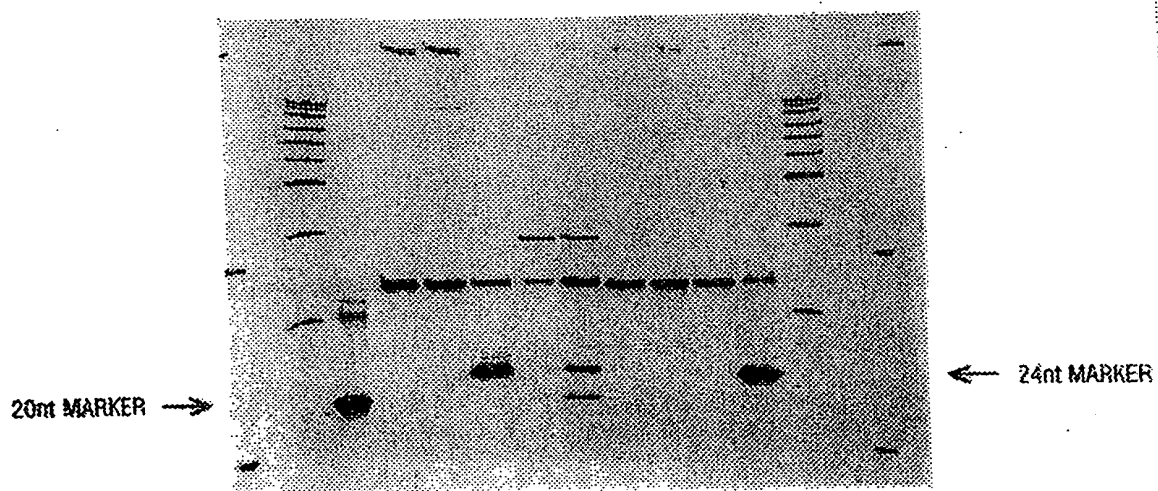


FIG. 24

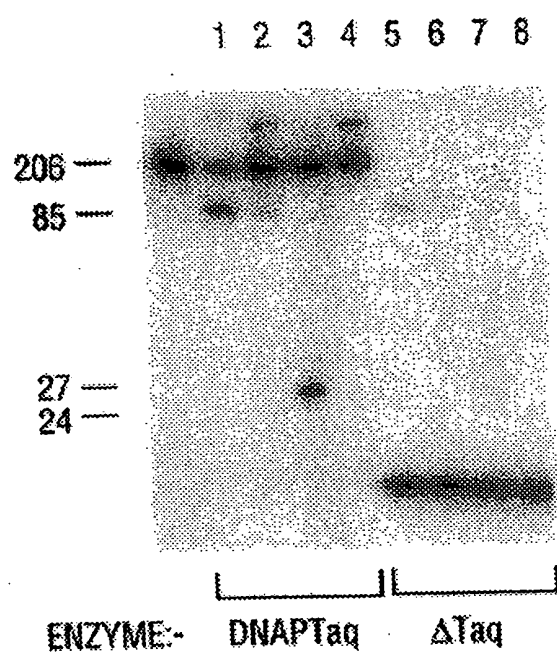


FIG. 25A

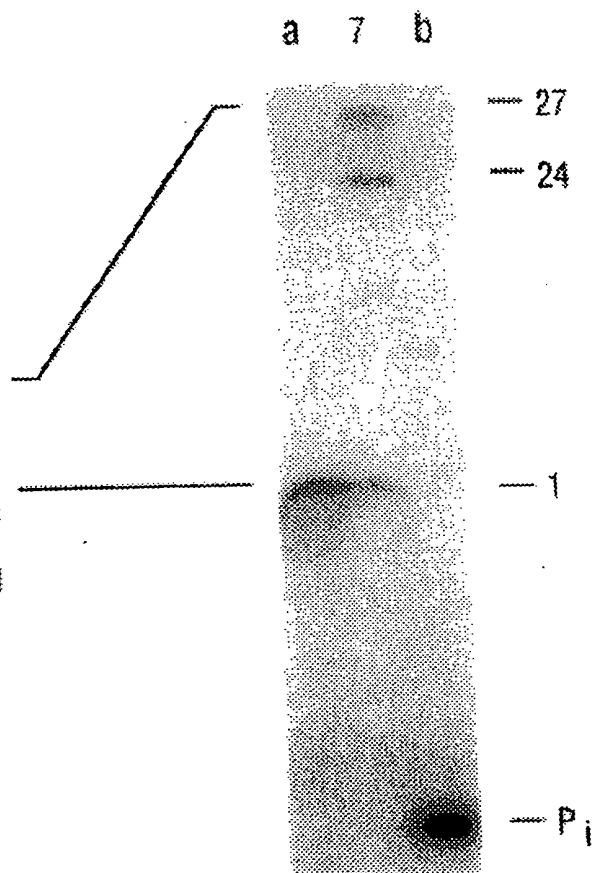


FIG. 25B

FIG. 26A

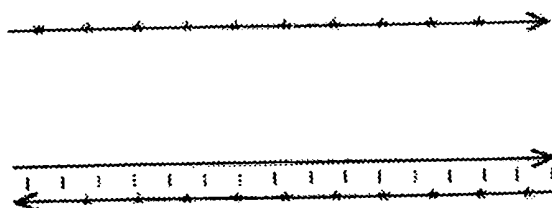
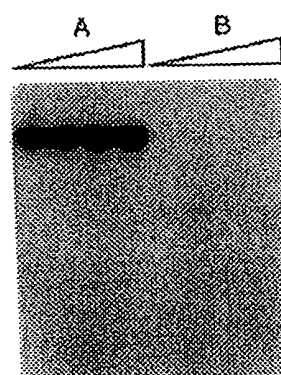


FIG. 26B

* = 32p



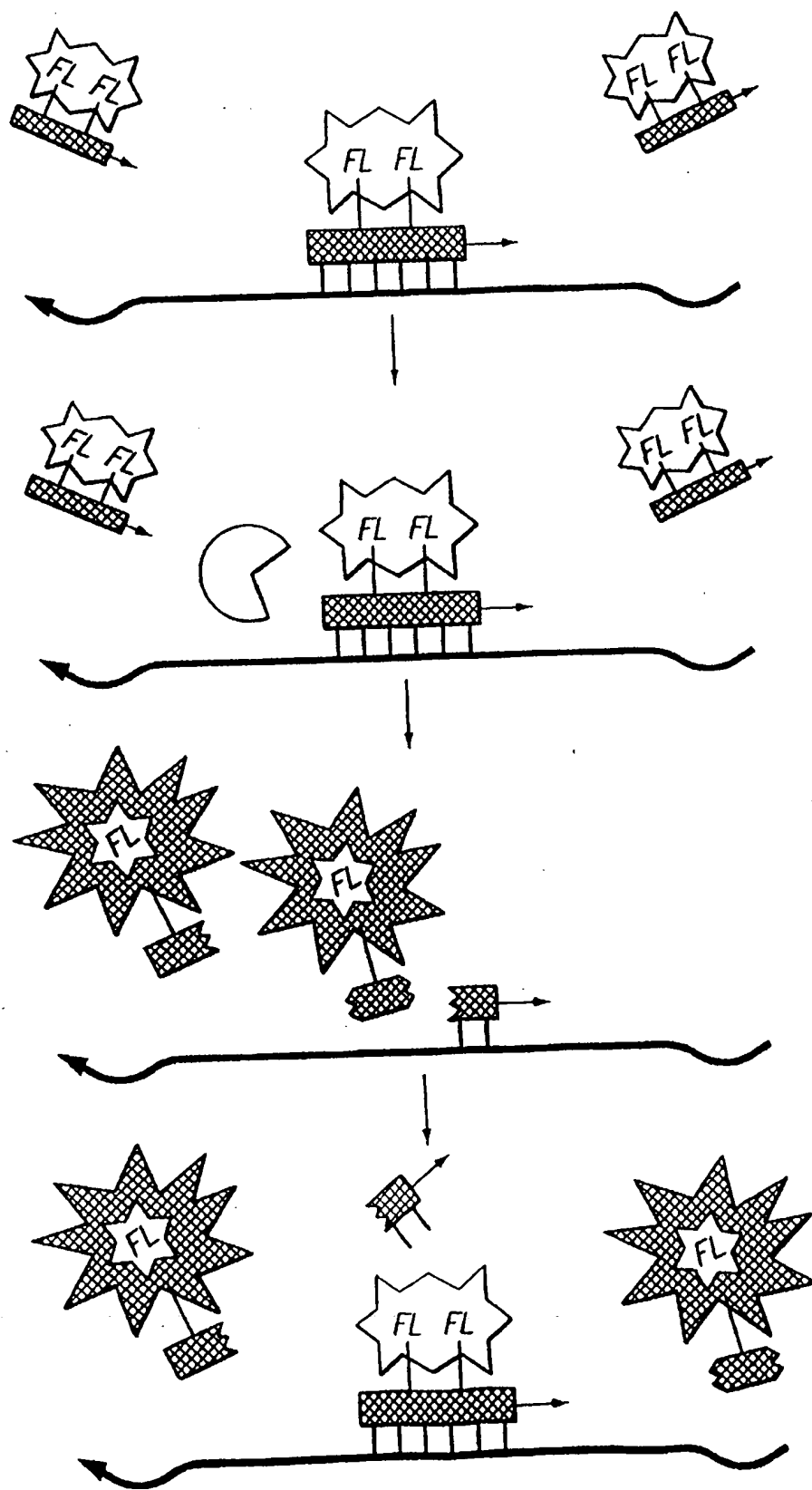


FIG. 27

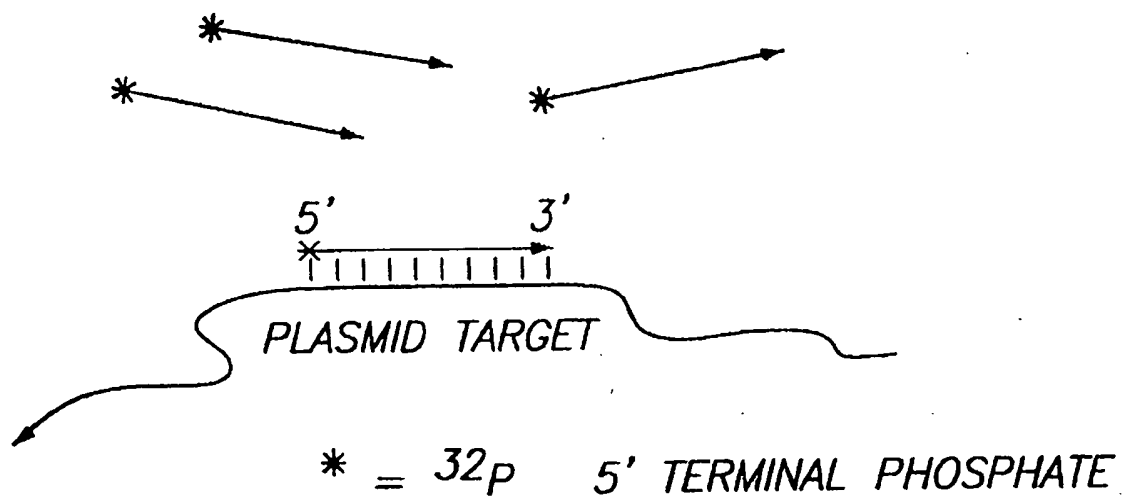


FIG. 28A

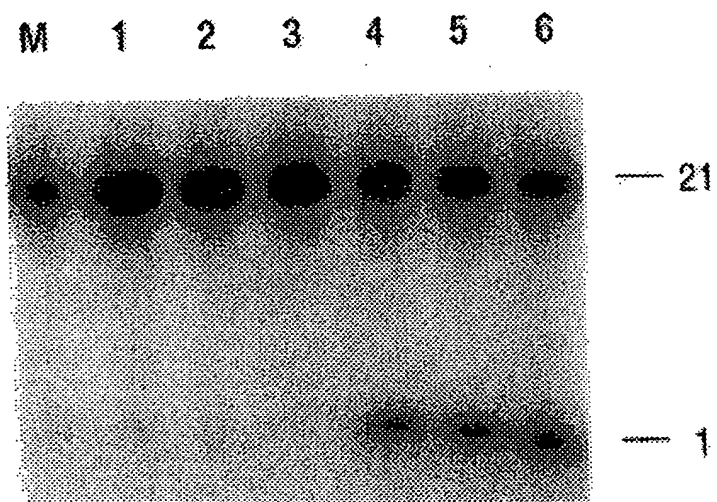


FIG. 28B

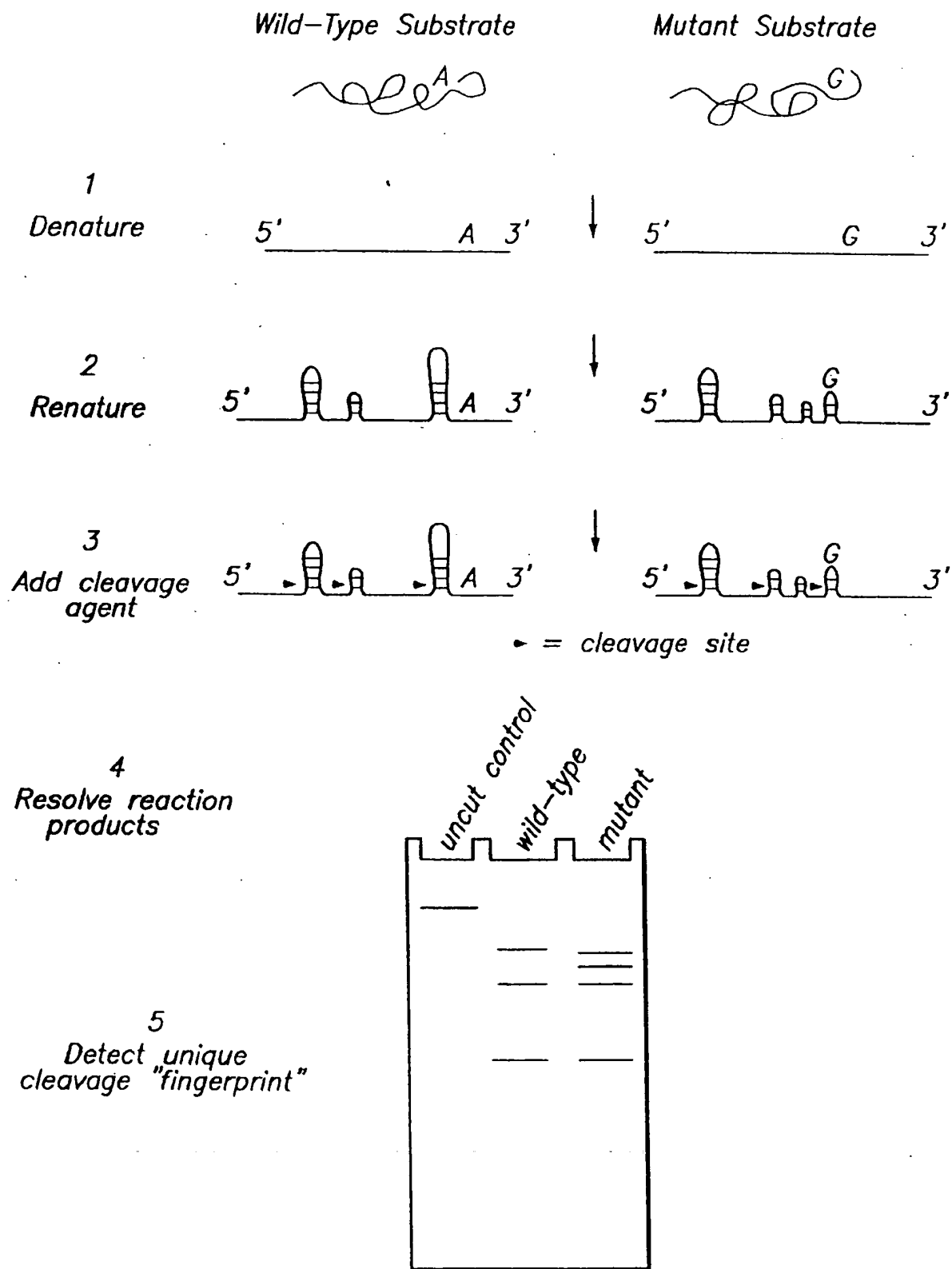


FIG. 29

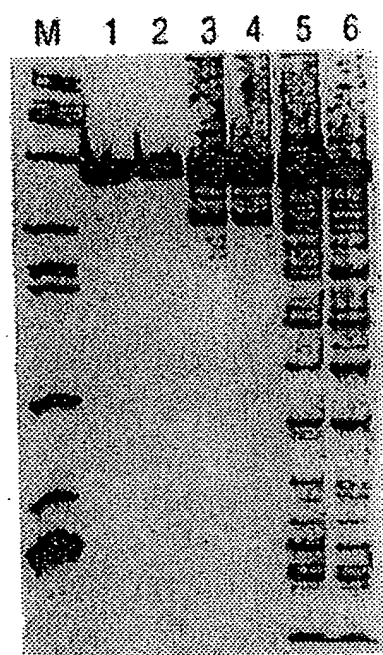


FIG. 30

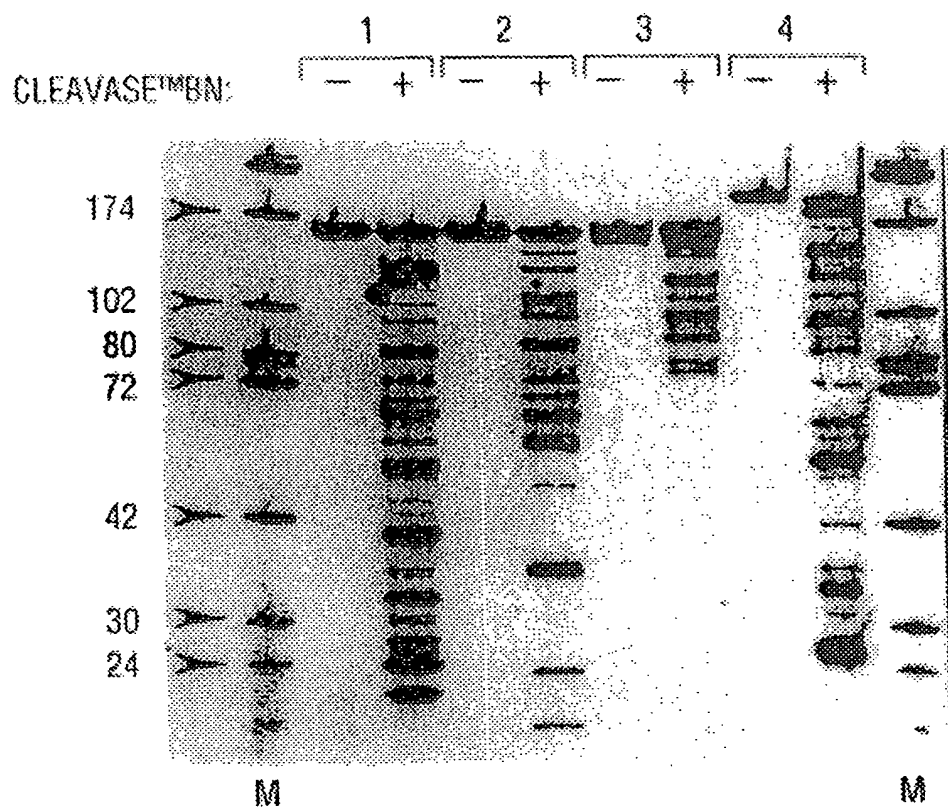


FIG. 31

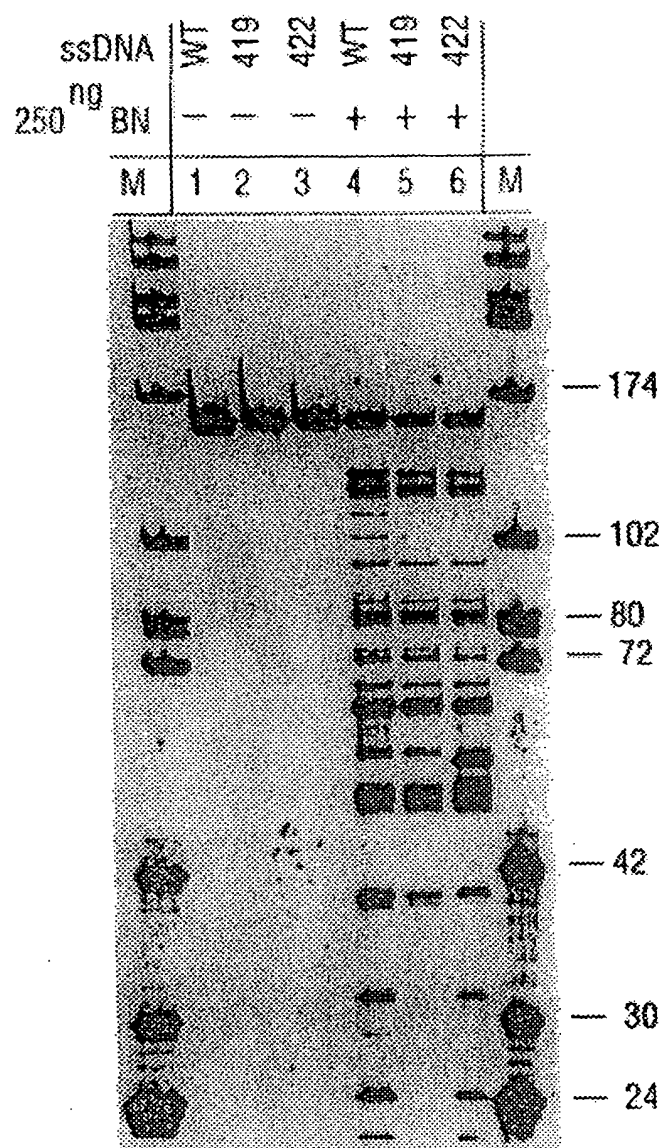
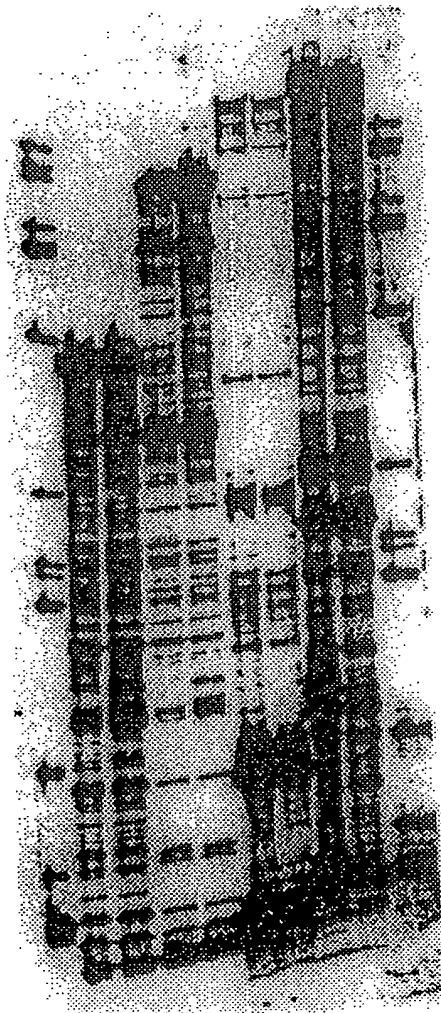


FIG. 32

157 378 1056 1587
M 1 2 3 4 5 6 7 8 M



WT 422 WT 422 WT 422 WT 422

FIG. 33

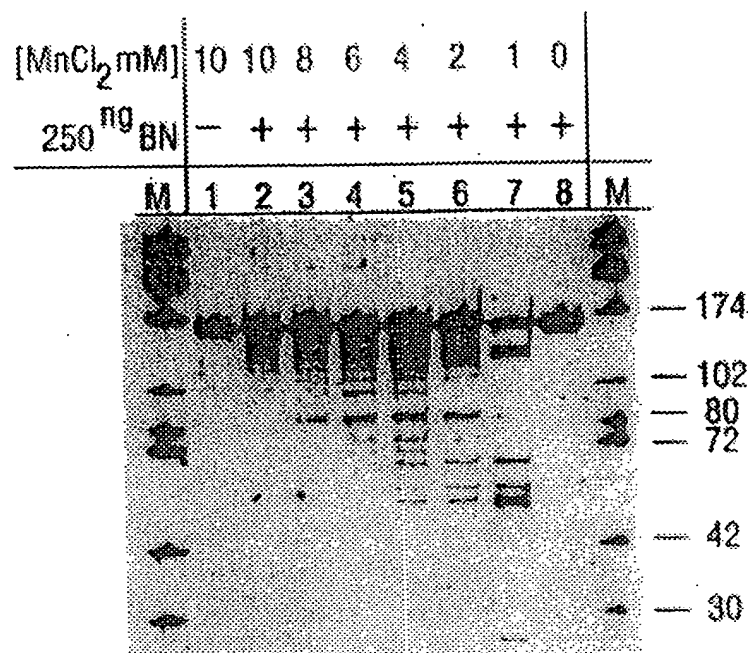


FIG. 34

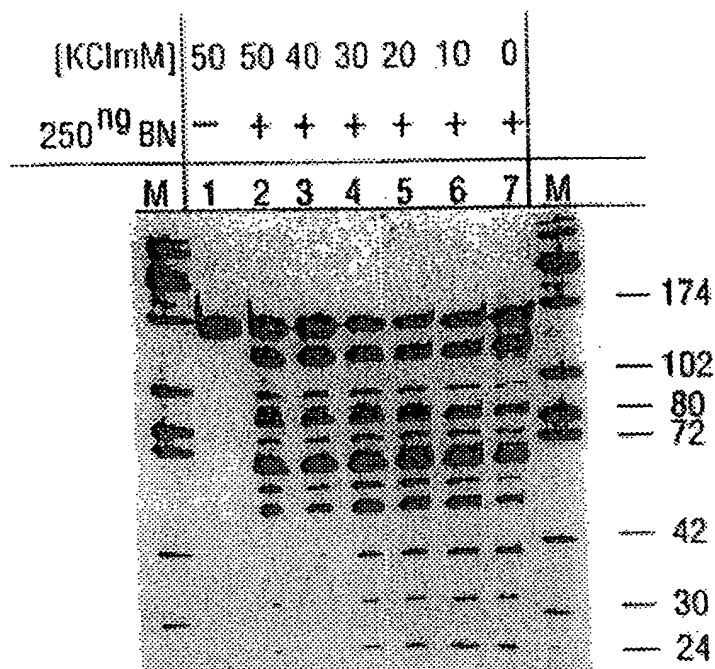


FIG. 35

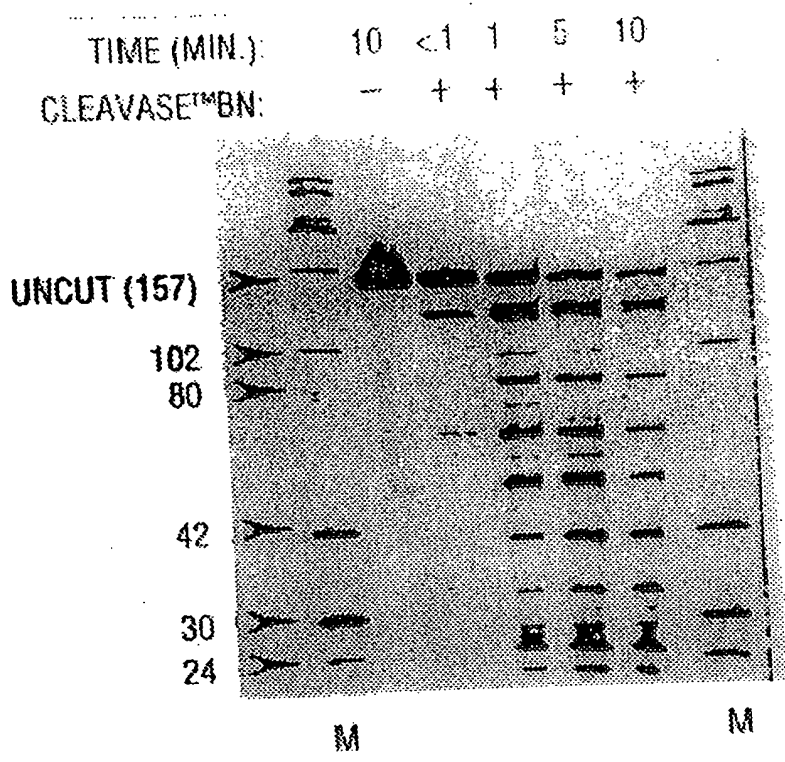


FIG. 36

TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	-	-	+	+	+	+	-	+

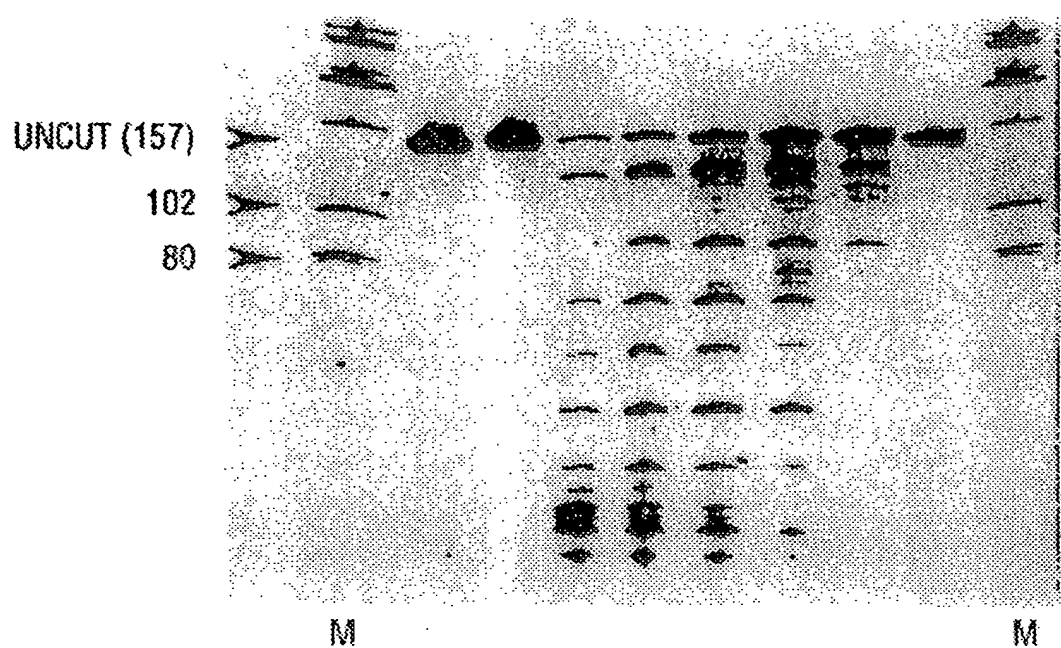


FIG. 37

CLEAVASETMBN (ng): — 10 50 100 250

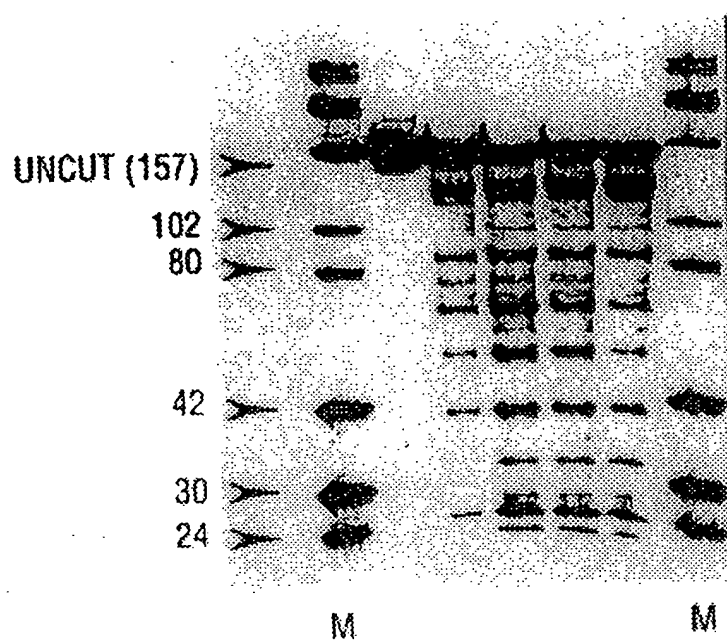


FIG. 38

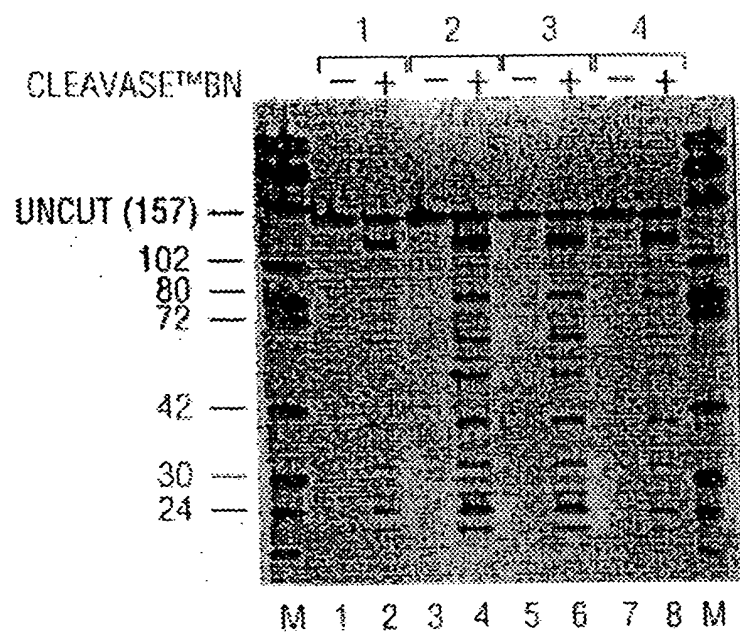


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA	WT	419	422	WT	419	422	WT	419	422	WT	419	422
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

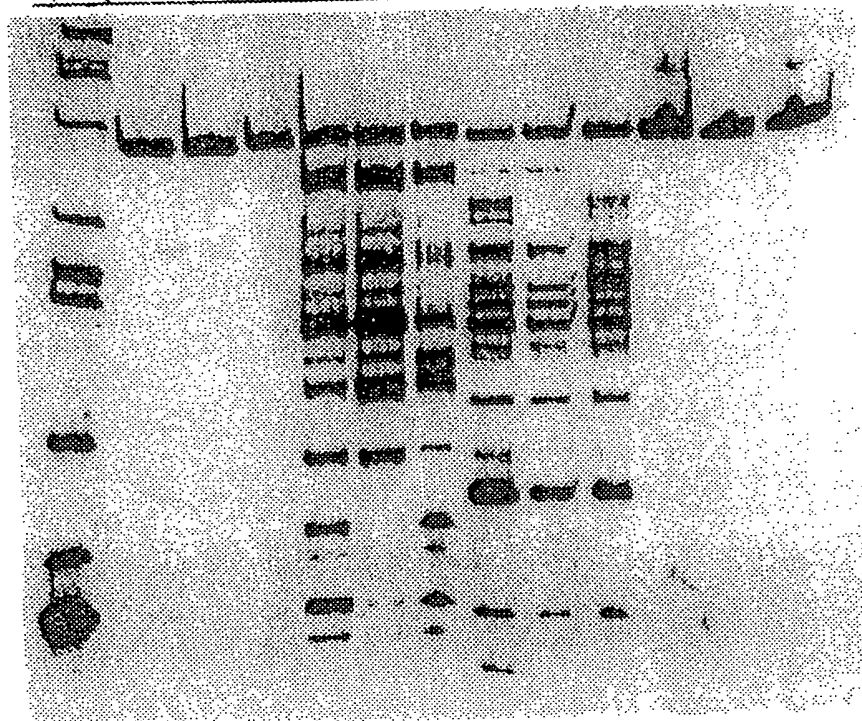


FIG. 40

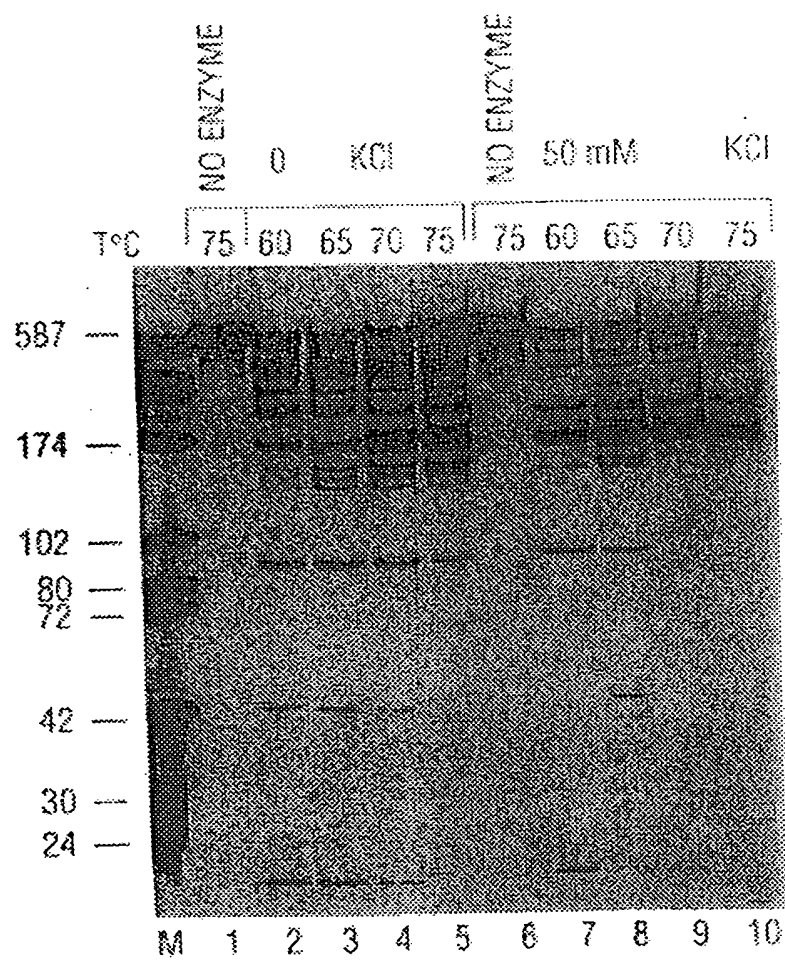


FIG. 41

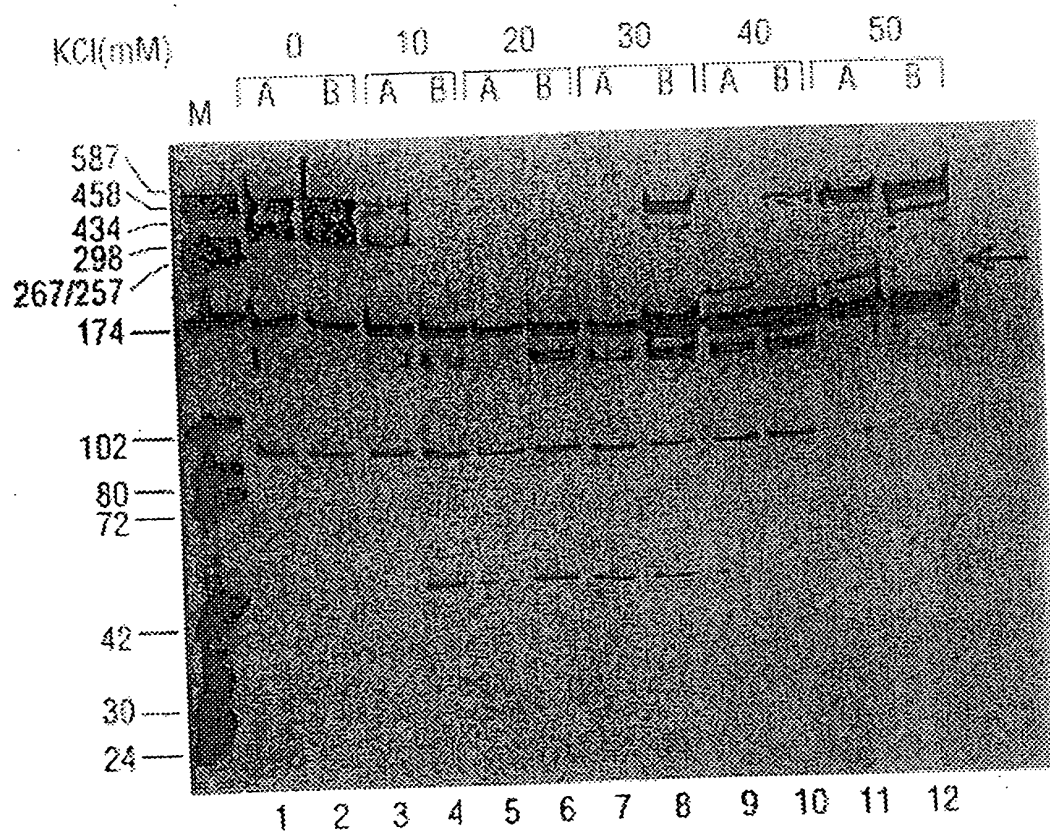


FIG. 42

CLEAVASE™BN

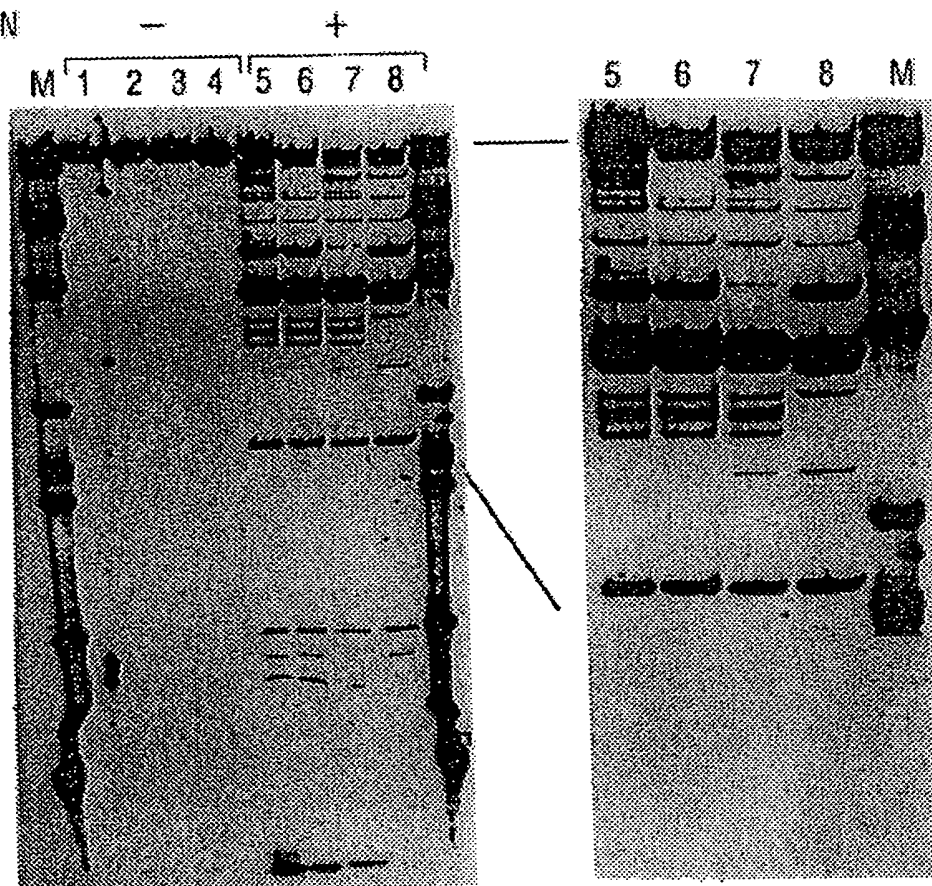


FIG. 43

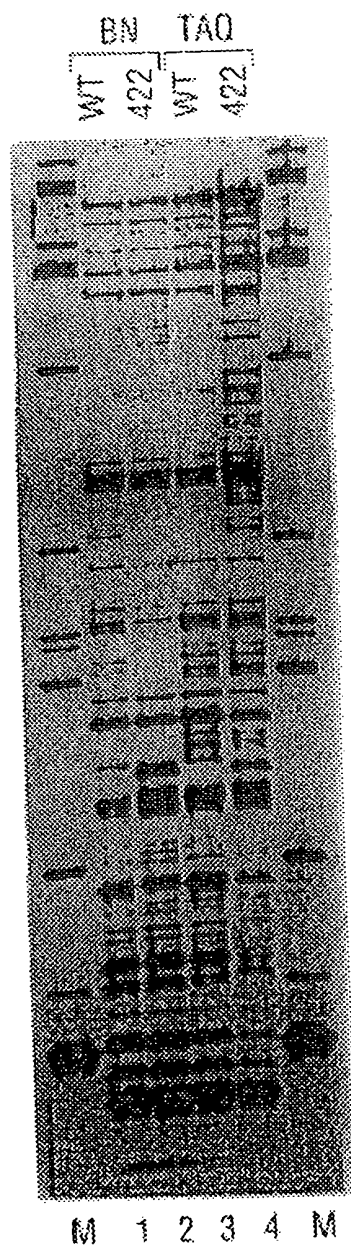


FIG. 45

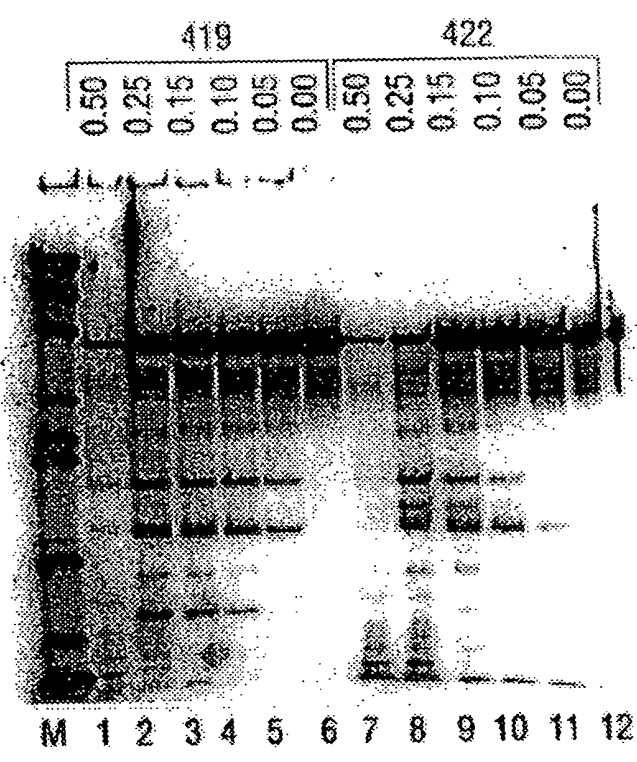


FIG. 47

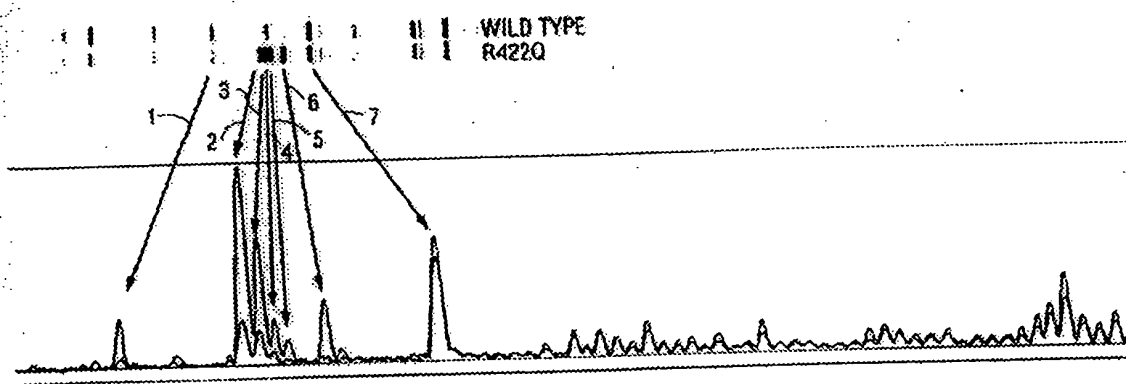


FIG. 48

L.100.8-1
(SEQ ID NO: 76) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10
(SEQ ID NO: 77) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12
(SEQ ID NO: 78) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3
(SEQ ID NO: 79) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251
(SEQ ID NO: 80) 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3
(SEQ ID NO: 81) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCTTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

L.100.8-1 (SEQ ID NO: 76)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA 100
L.46.16-10 (SEQ ID NO: 77)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGTGAAAGA
L.46.16-12 (SEQ ID NO: 78)	ATGTTATGGGGAGG-----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC-----TCGGCCAGCCCTTGTTGGTGAAAGA
L19.16-3 (SEQ ID NO: 19)	ATGTTACGGGGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGGAGAGA
L.CEM/251 (SEQ ID NO: 80)	ATGTTACGGGGAGGTACTGGGAAGGAGCCGGTCGGGAACGCCCACTTTCT TACAATGCCCCCTCCATGACCCCTTCTCGGCCAGCCCTTGCGGGTGAAAGA
L.36.8-3 (SEQ ID NO: 81)	ATGTTACGGGAGAGGTACTGGGGAGGAGCCGGTCGGGAACGCCCACTCTCT TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA

FIG. 49B

150

L.100.8-1

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.46.16-10

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.46.16-12

5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.19.16-3

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.CEM/251

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

L.36.8-3

5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTCAGTCGCTCTGCGGA
3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAGCGAGACGCCT

FIG. 49C

200

L.100.8-1

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-10

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-12

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.19.16-3

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.CEM/251

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.36.8-3

GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC

FIG. 49D

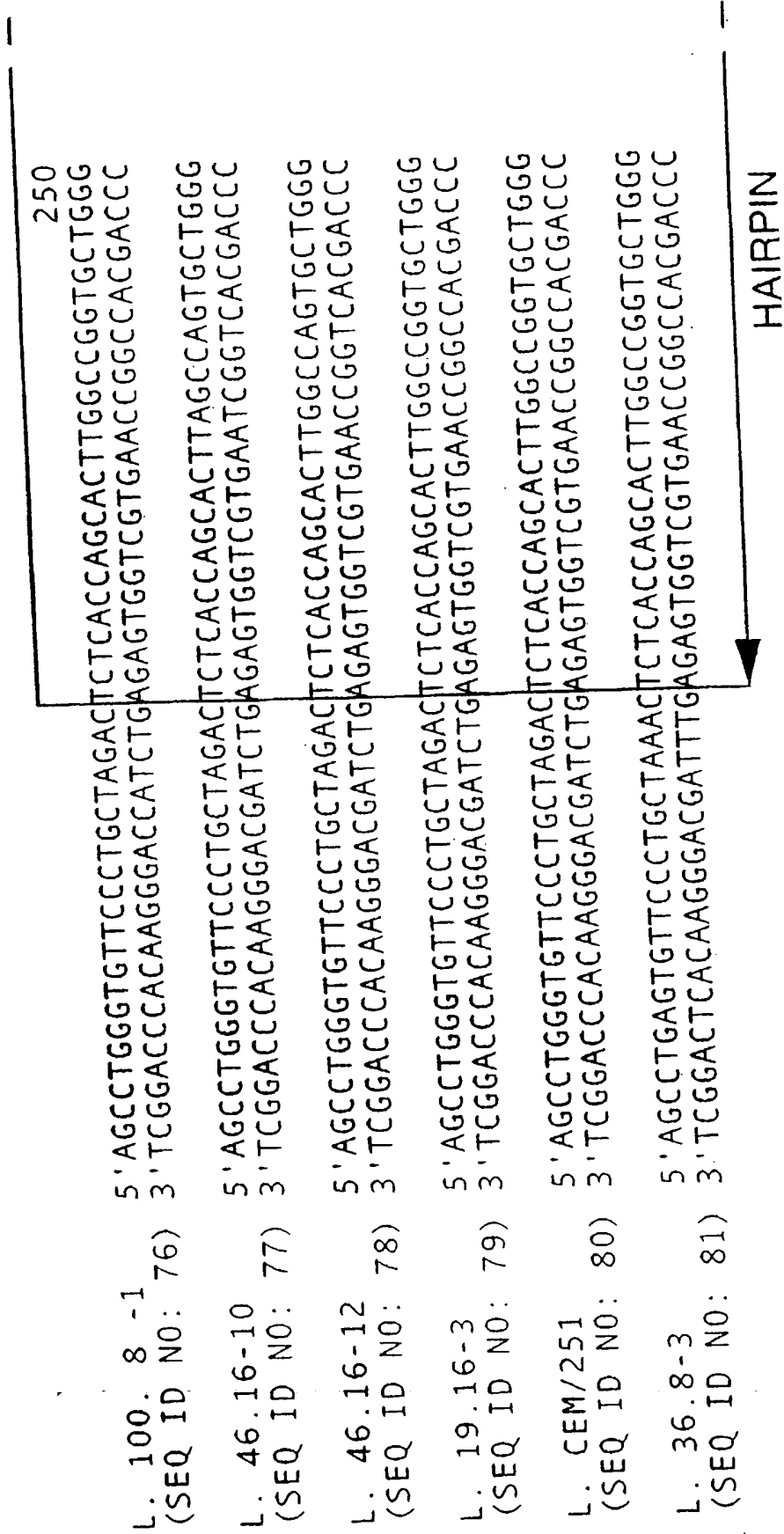


FIG. 49E

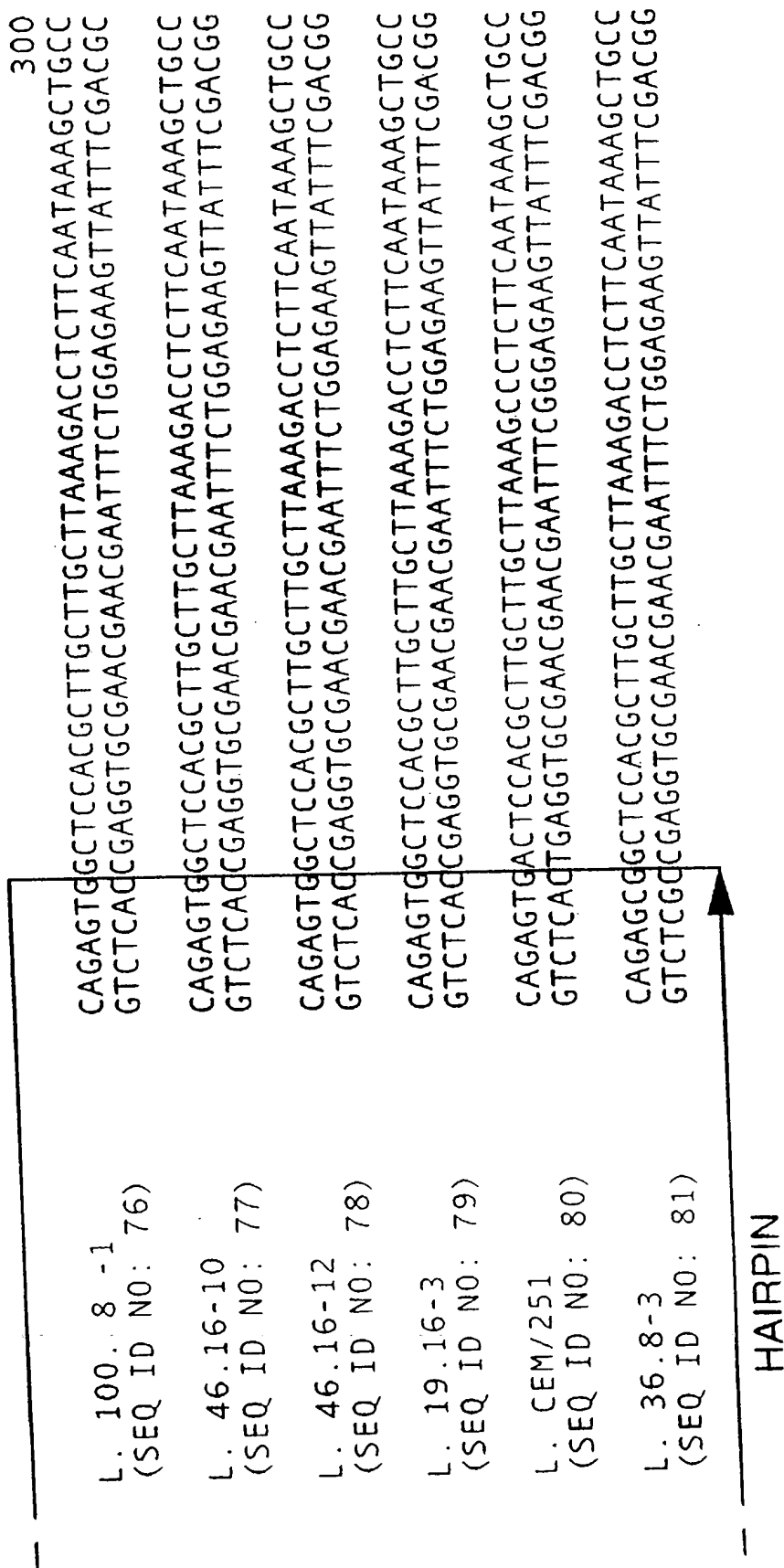


FIG. 49F

L.100.8-1	<div>350</div> 5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG G 3' 3'TAAATCTTCATCCGGTCACACACAAGGTTAGAGAGGATCGGCGCGGAC C 5'
L.46.16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG G 3' 3'TAAATCTTCATTCGGTCACACACAAGGTTAGAGAGGATCGGCGCGGAC C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG G 3' 3'TAAATCTTCATTCGGTCACACACAAGGTTAGAGAGGATCGGCGCGGAC C 5'
L.19.16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG G 3' 3'TAAATCTTCATCCGATCACACACAAGGTTAGAGAGGATCGGCGCGGAC C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG G 3' 3'TAAATCTTCATTCGATCACACACAAGGTTAGAGAGGATCGGCGCGGAC C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG G 3' 3'TAAATCTTCATCCGATCACACACAAGGTTAGAGAGGATCGGCGCGGAC C 5'

FIG. 49G

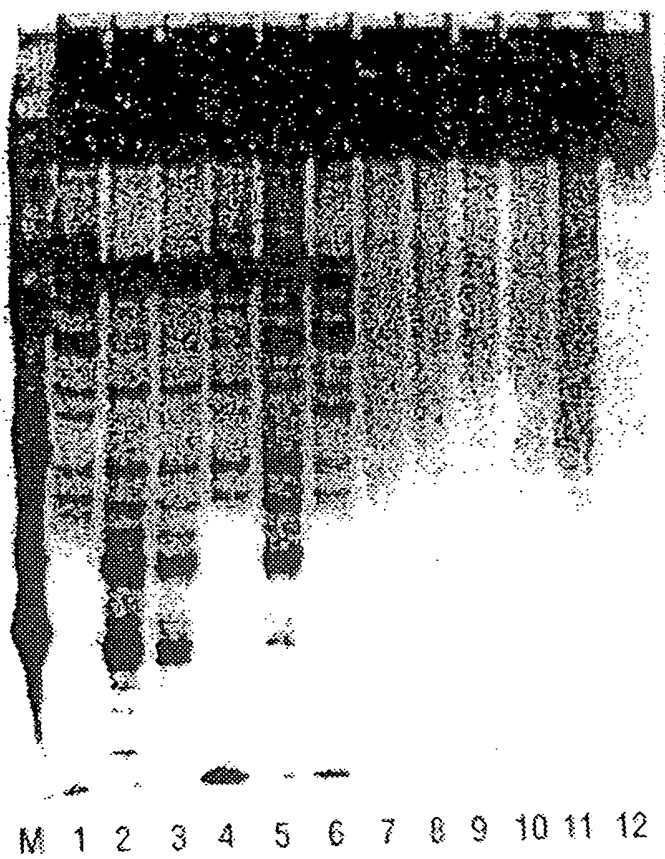


FIG. 50

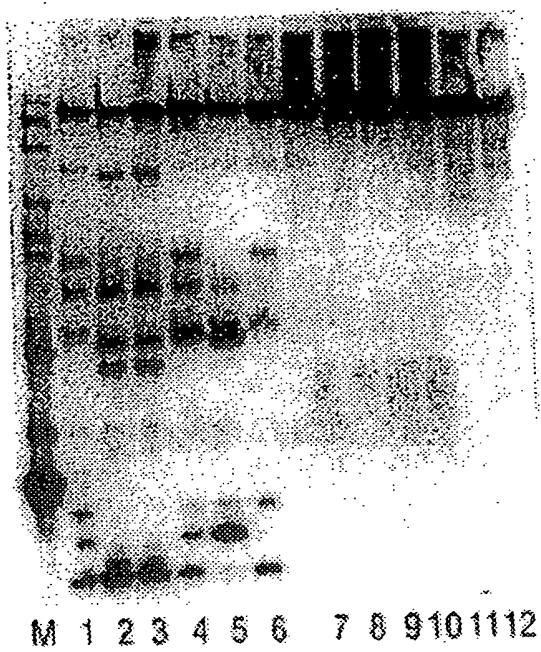


FIG. 51

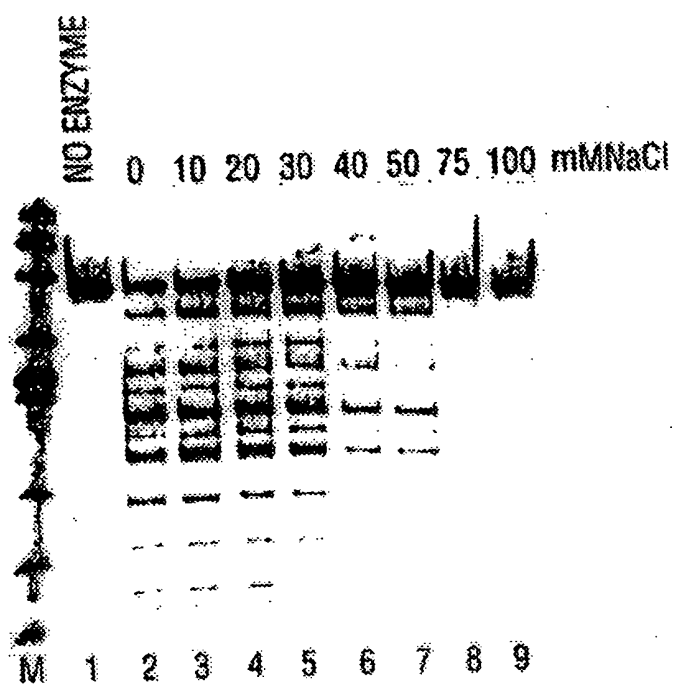


FIG. 52

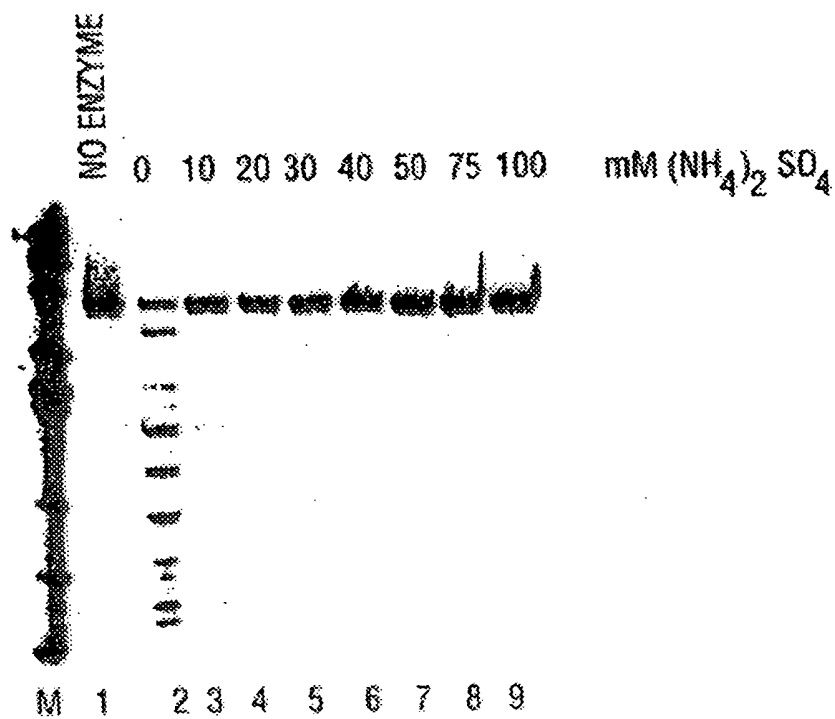


FIG. 53

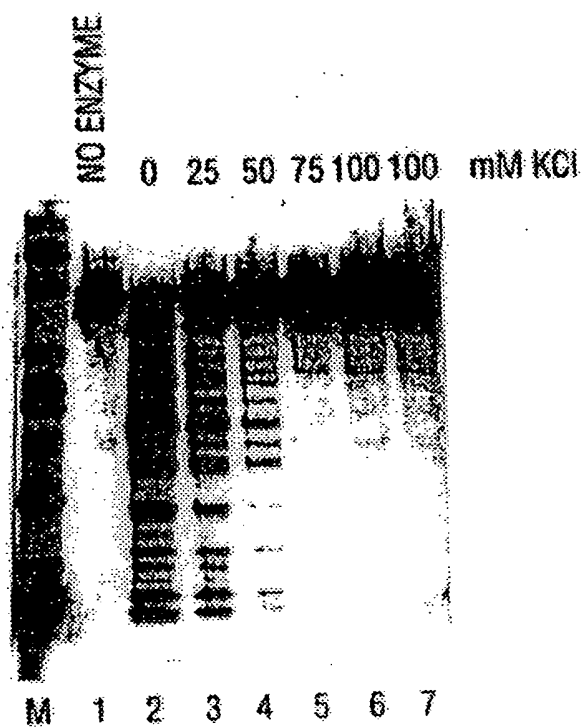


FIG. 54

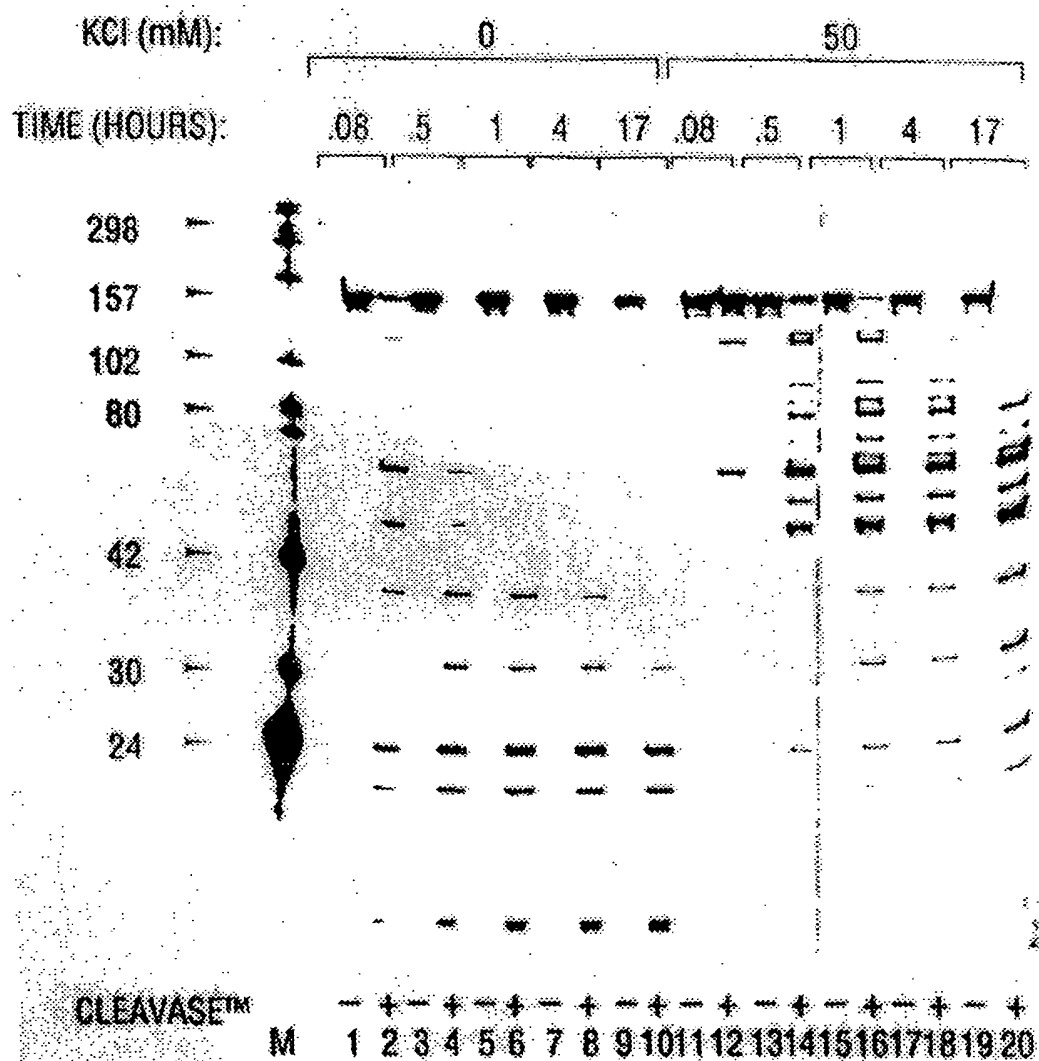


FIG. 55

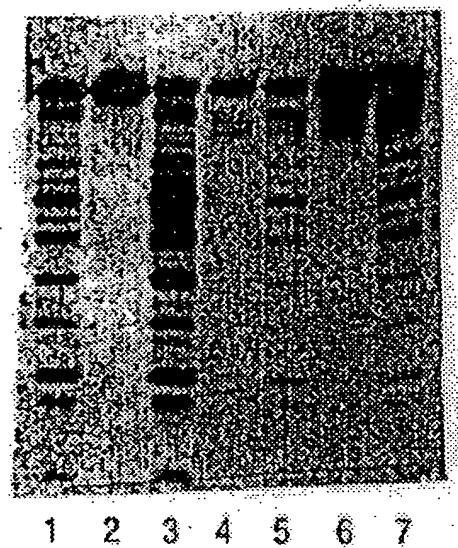


FIG. 56

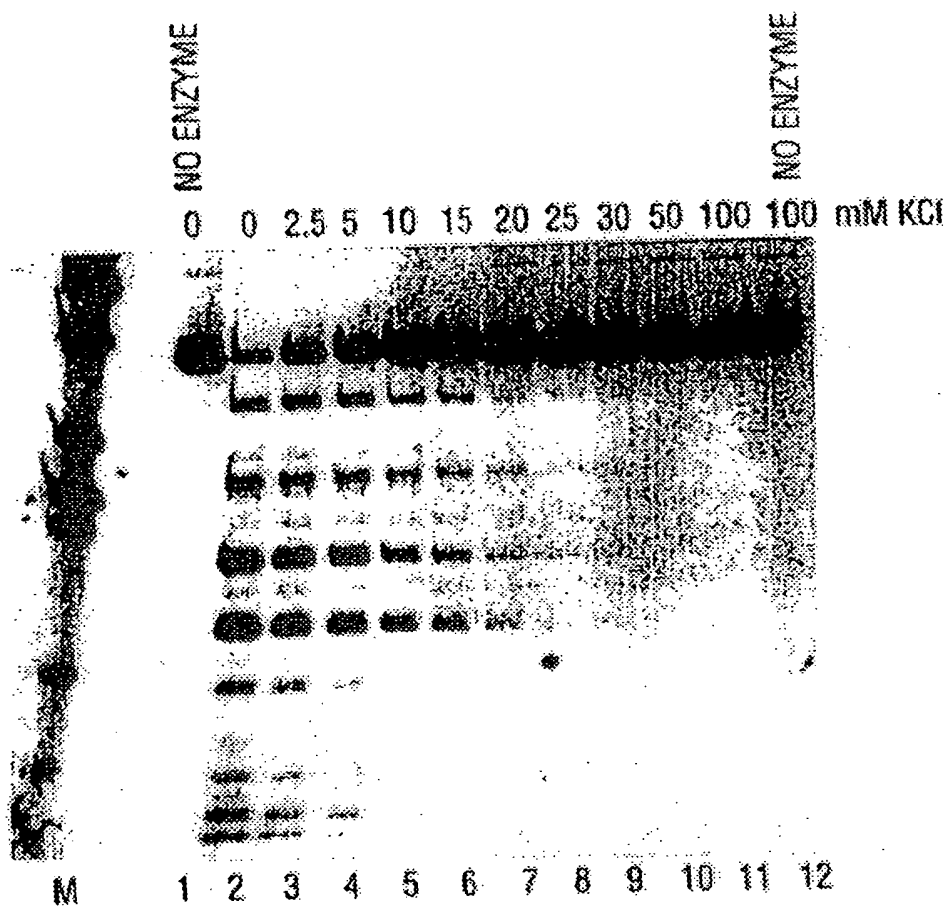


FIG. 57

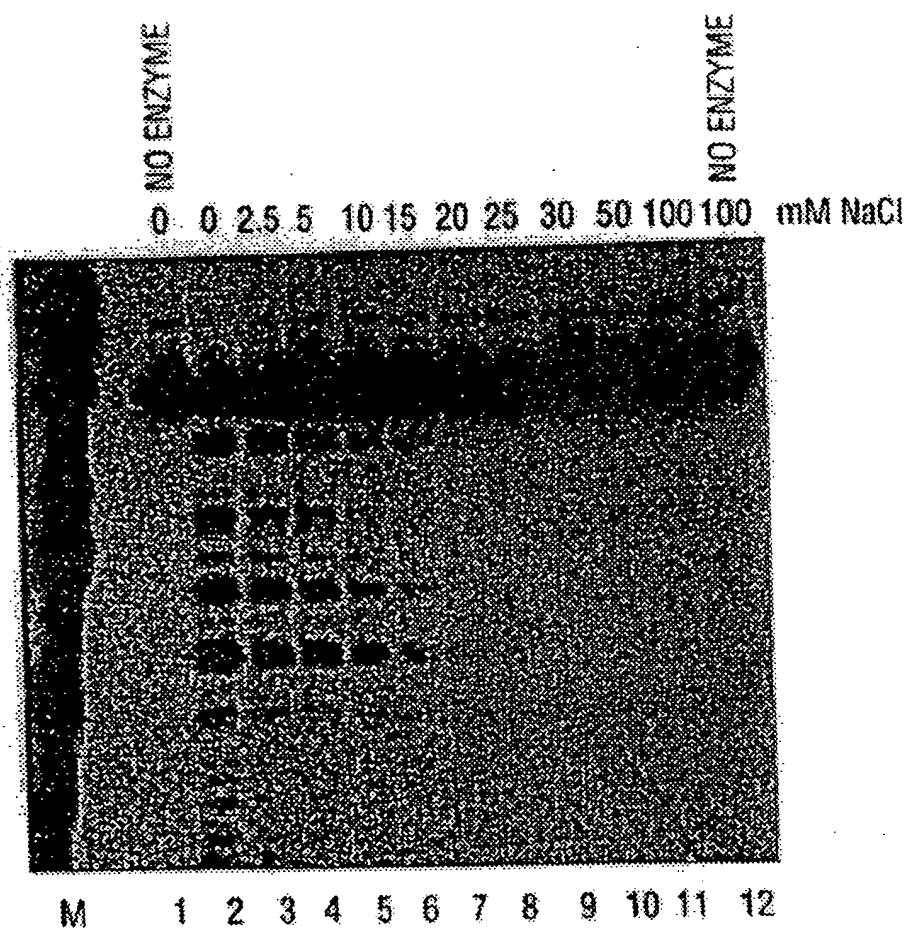


FIG. 58

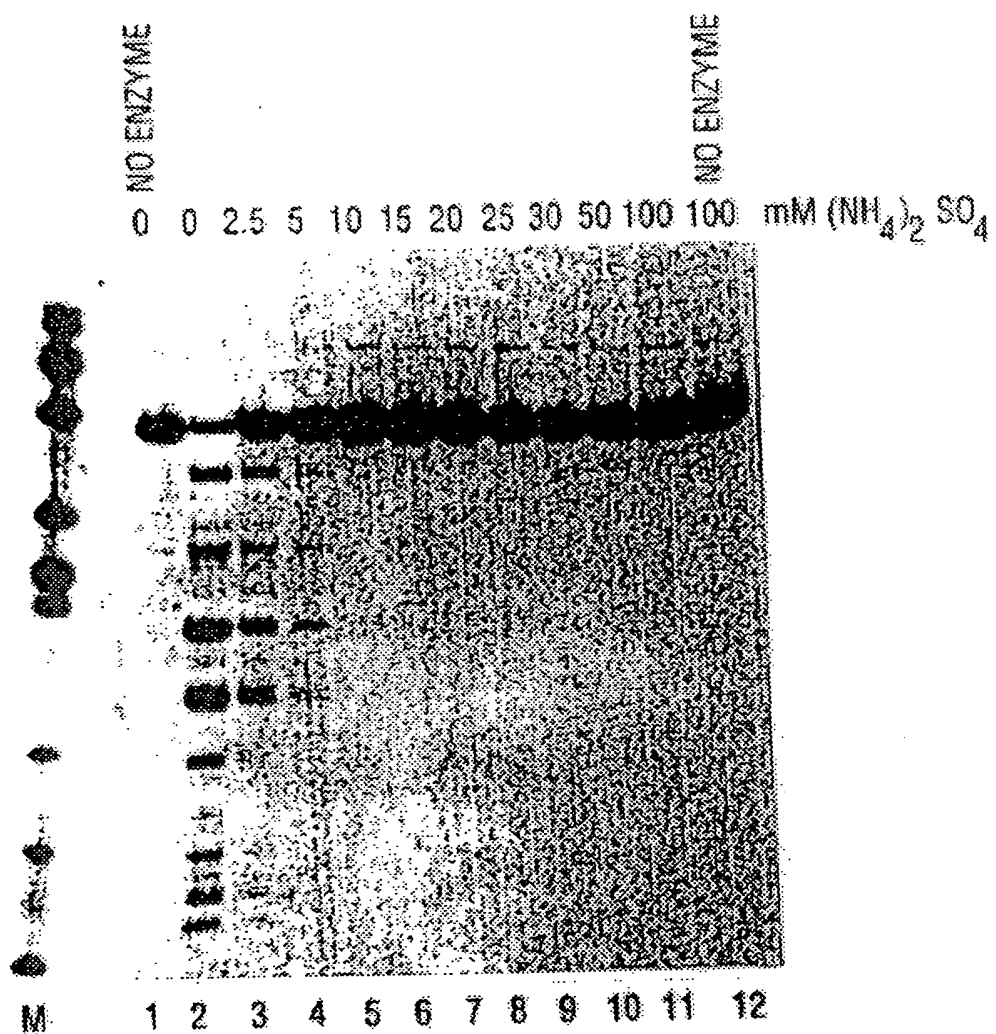


FIG. 59

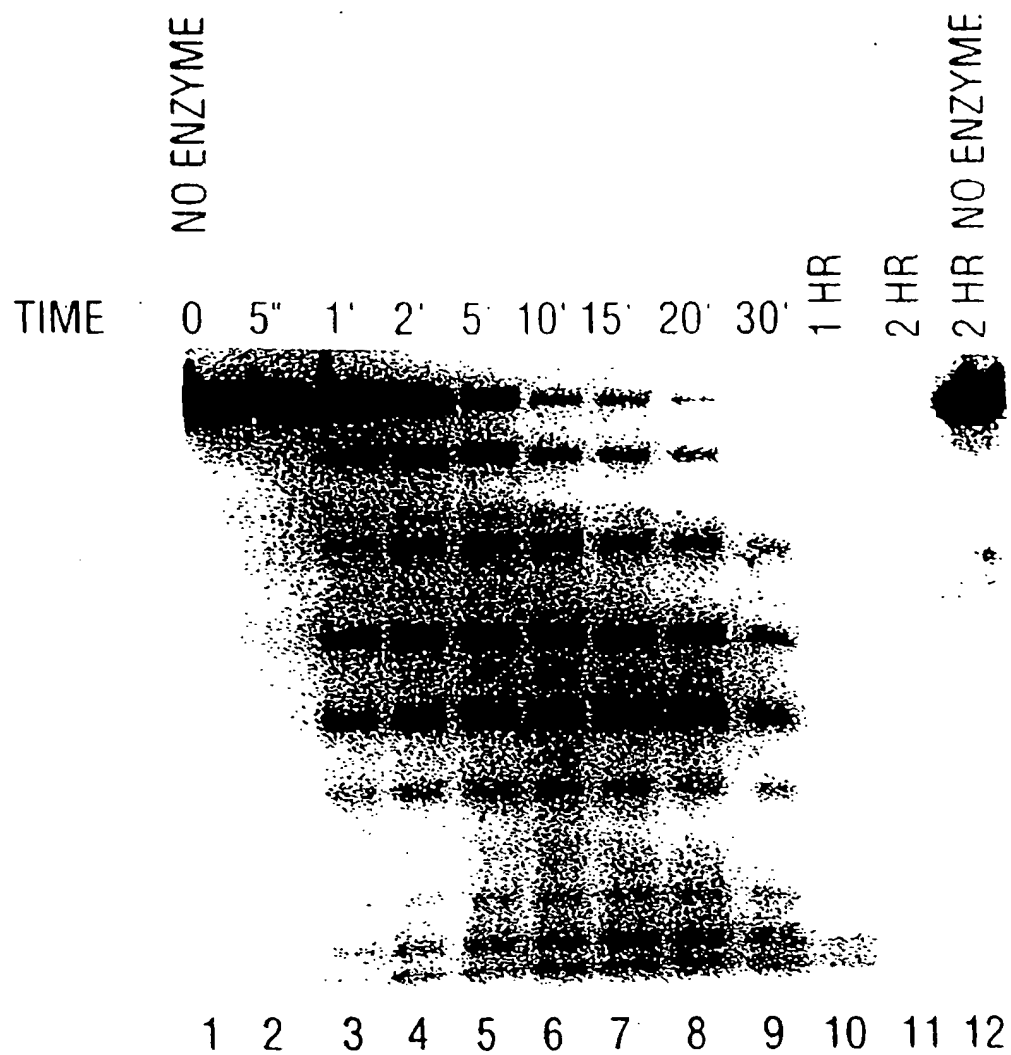


FIG. 60

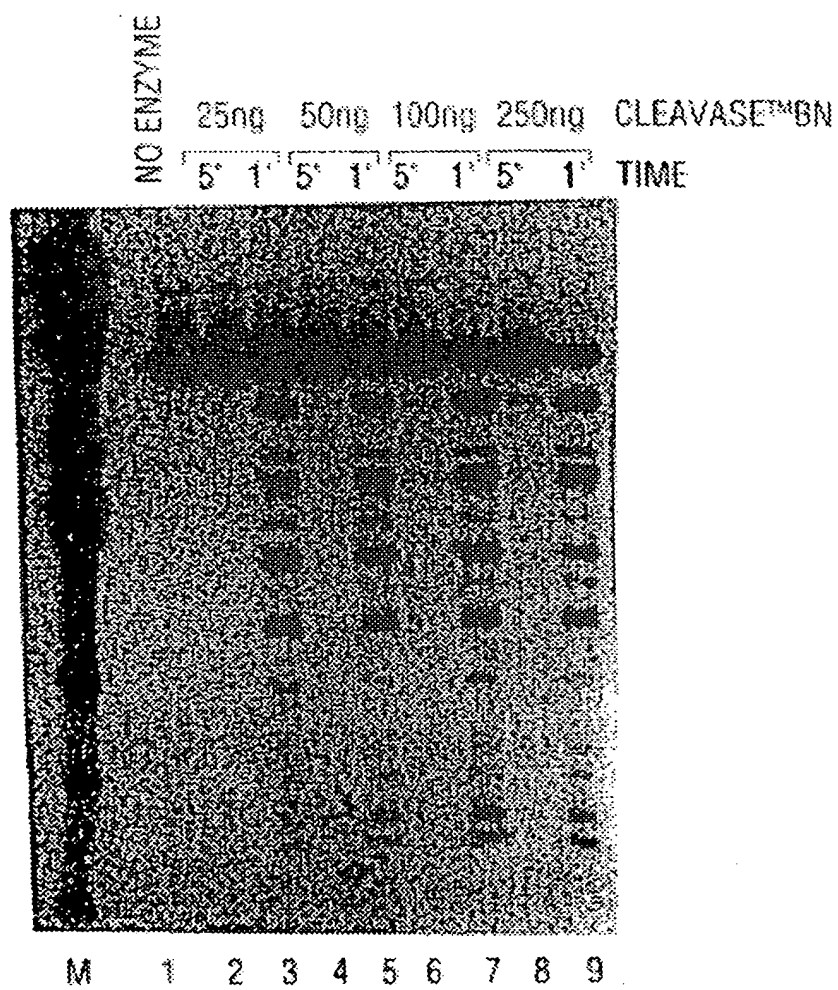


FIG. 61

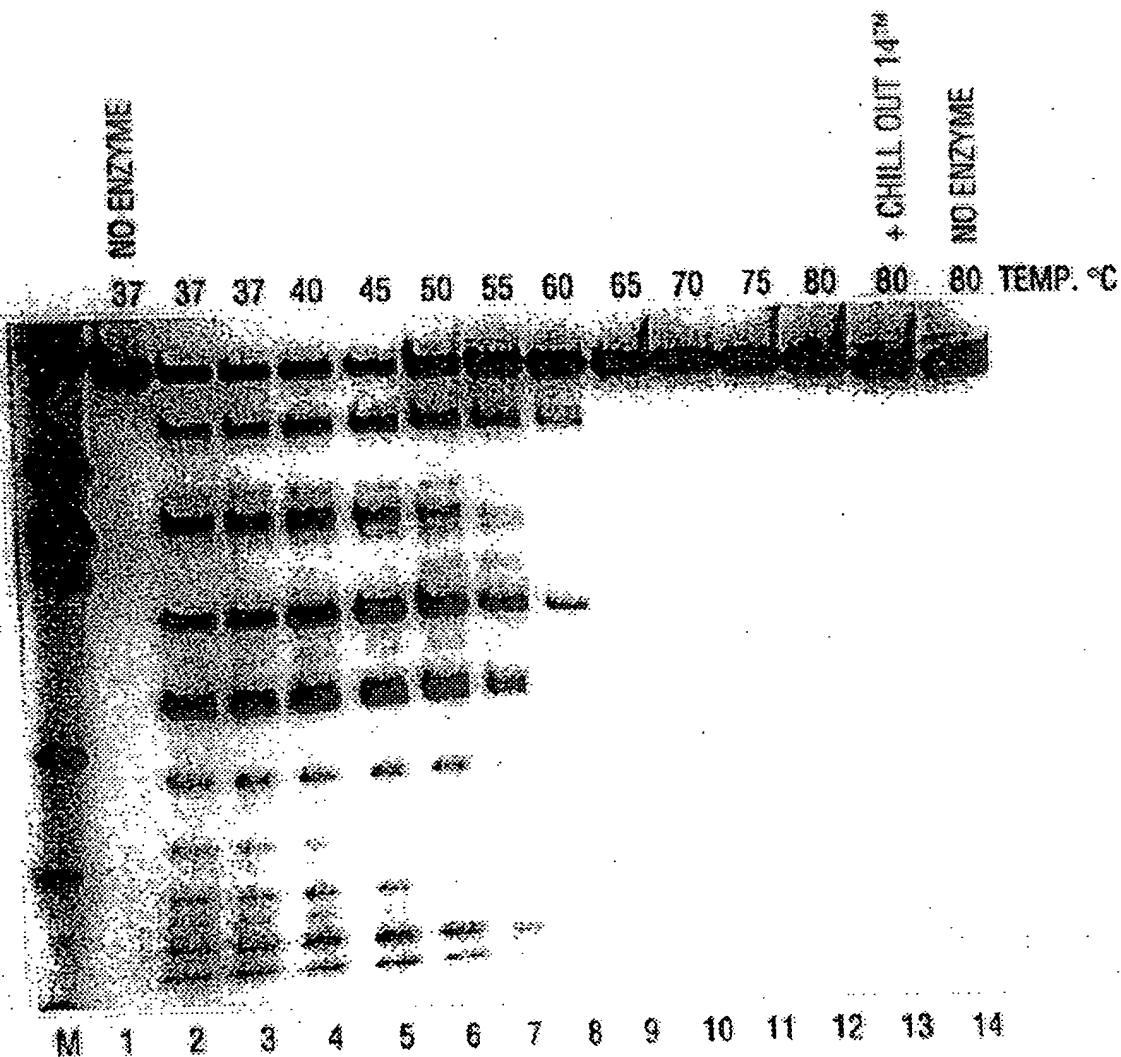


FIG. 62

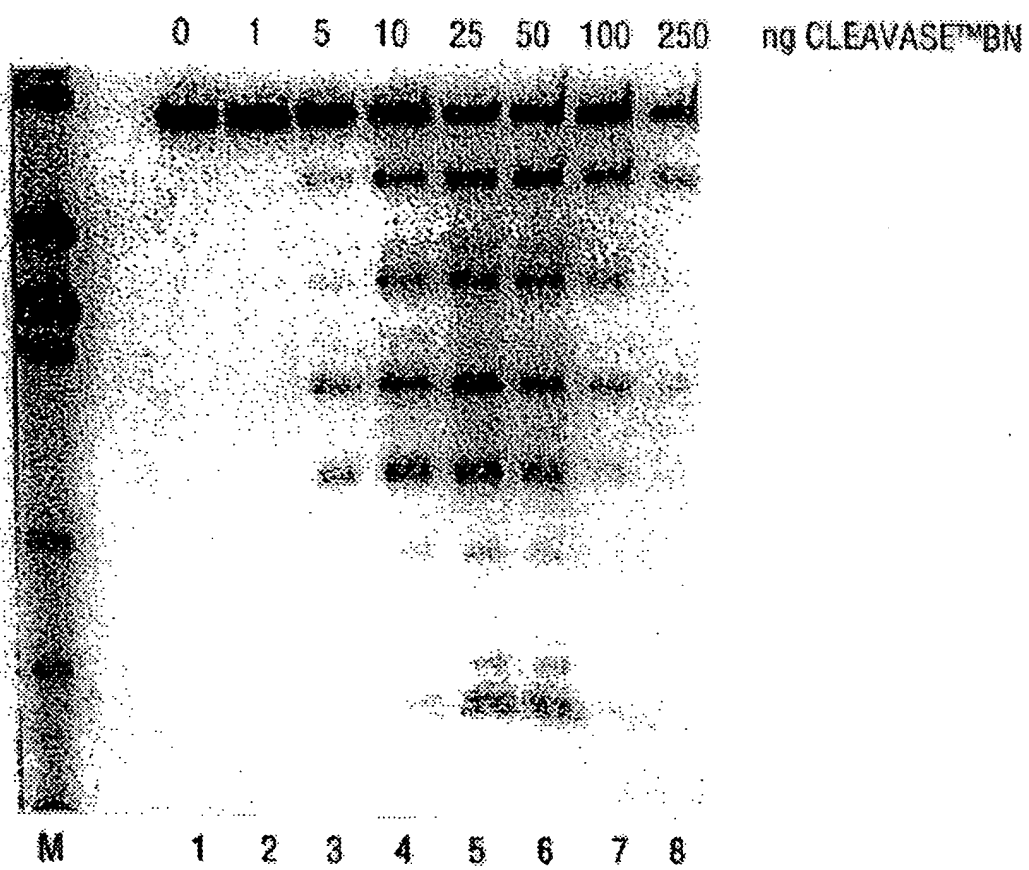


FIG. 63

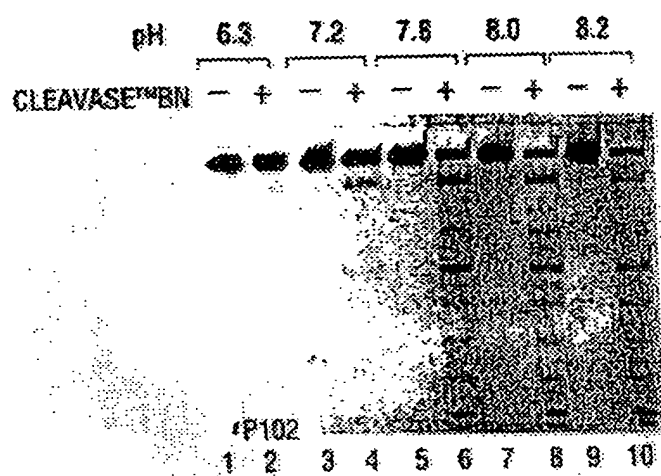


FIG. 64A

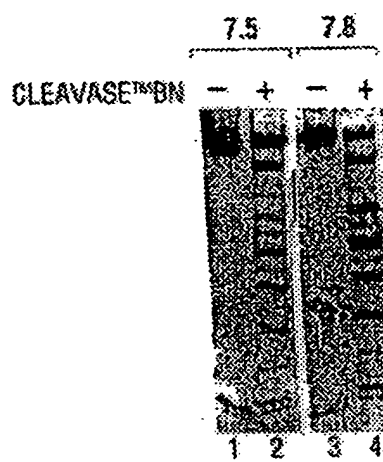


FIG. 64B

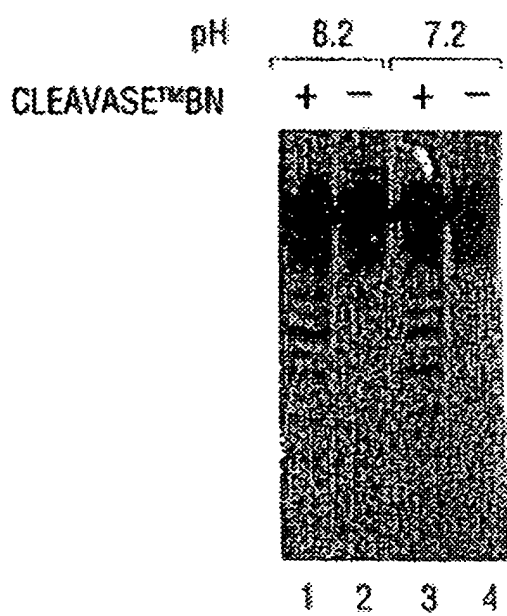


FIG. 65A

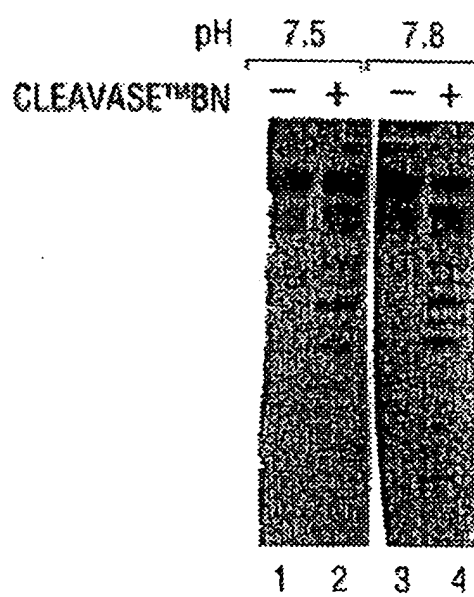


FIG. 65B

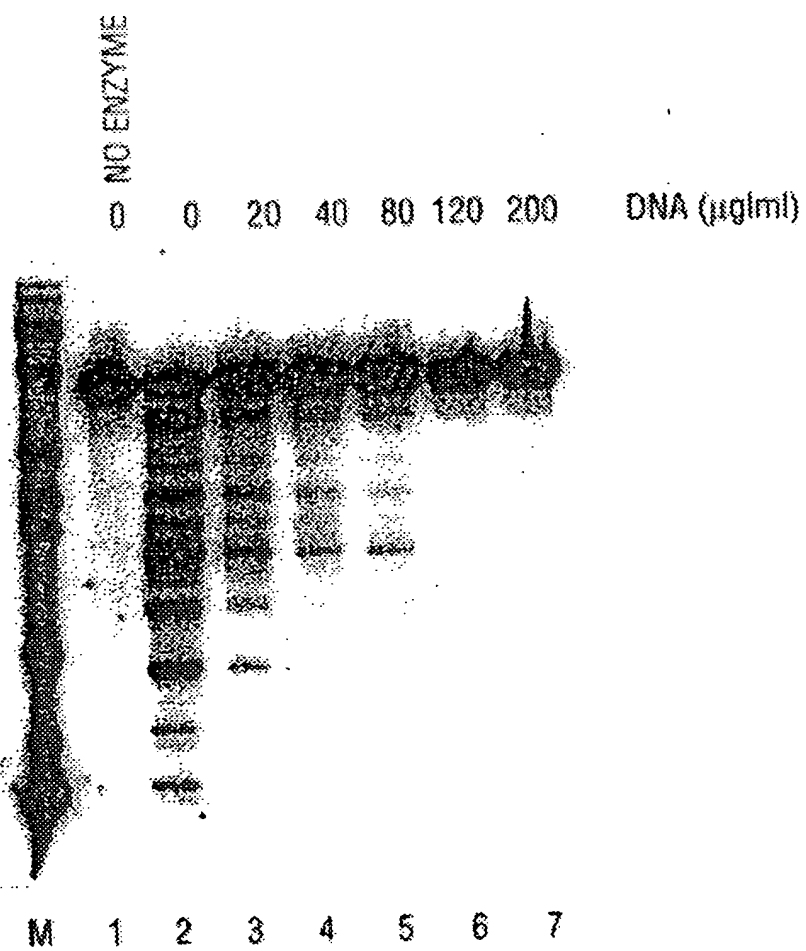


FIG. 66

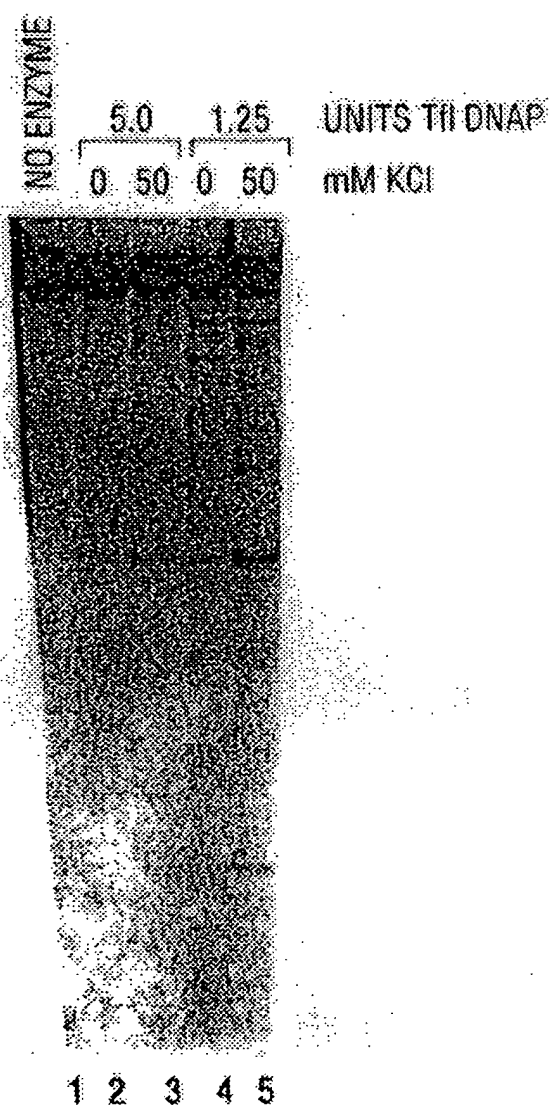


FIG. 67

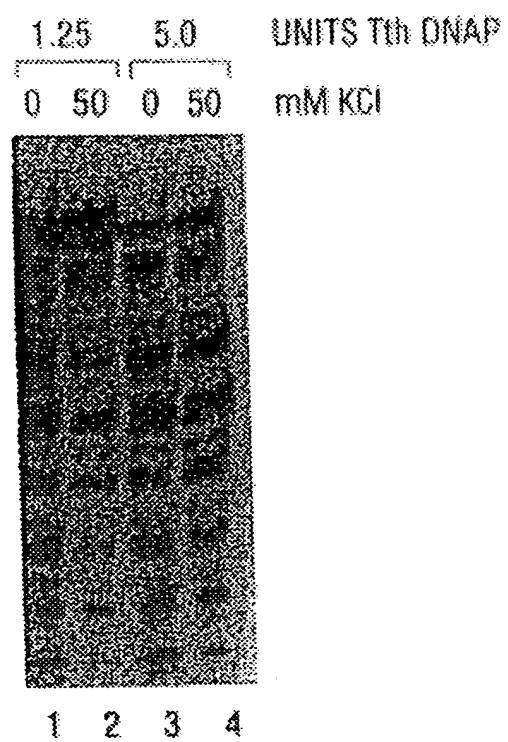


FIG. 68

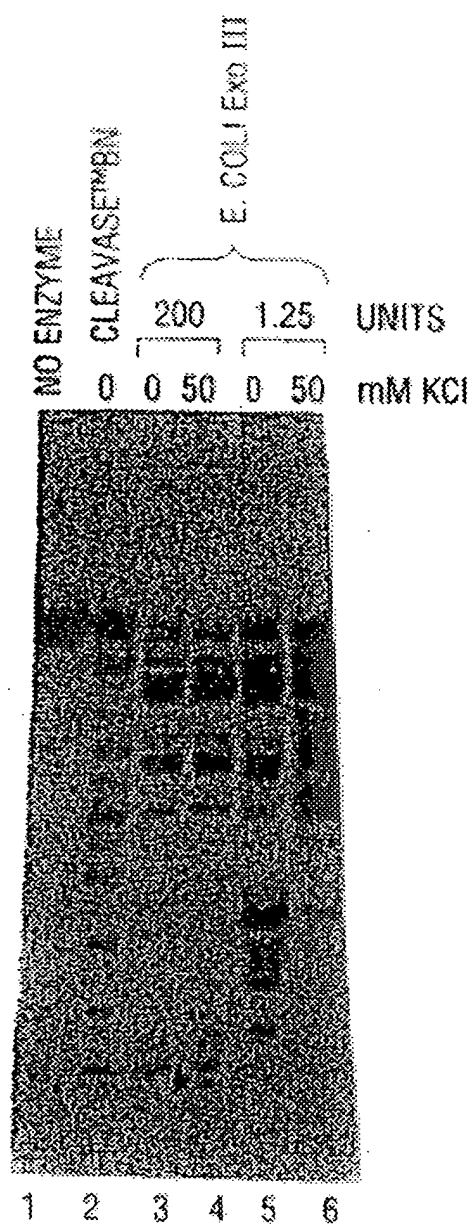


FIG. 69

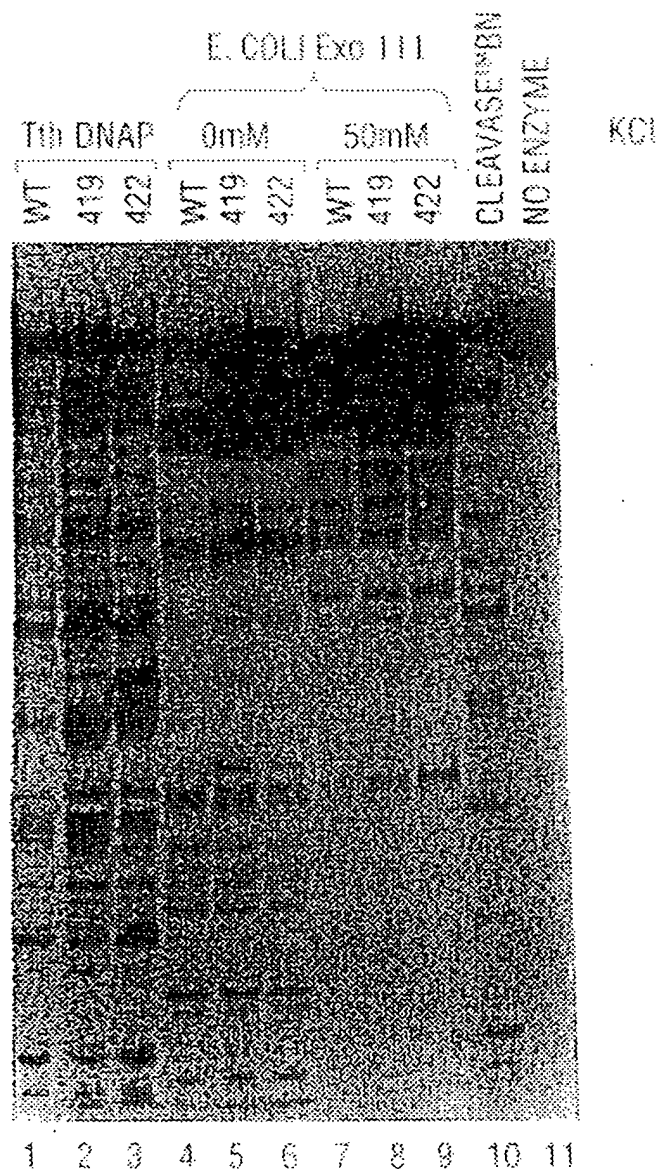
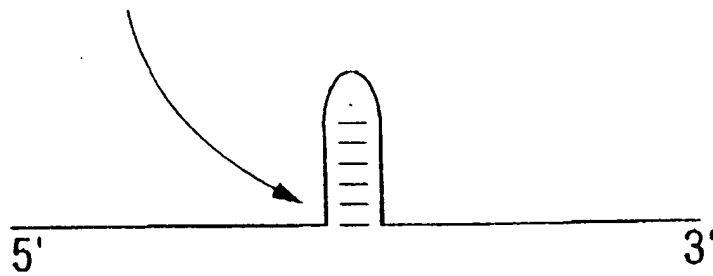


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

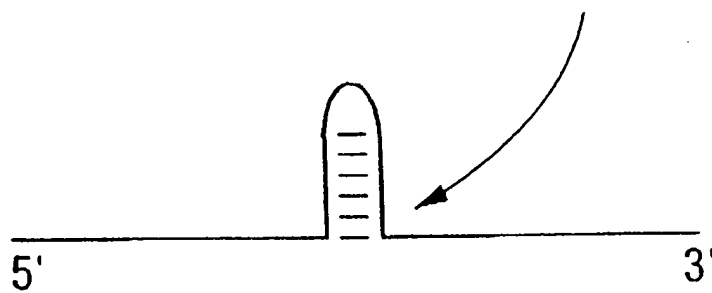


FIG. 71

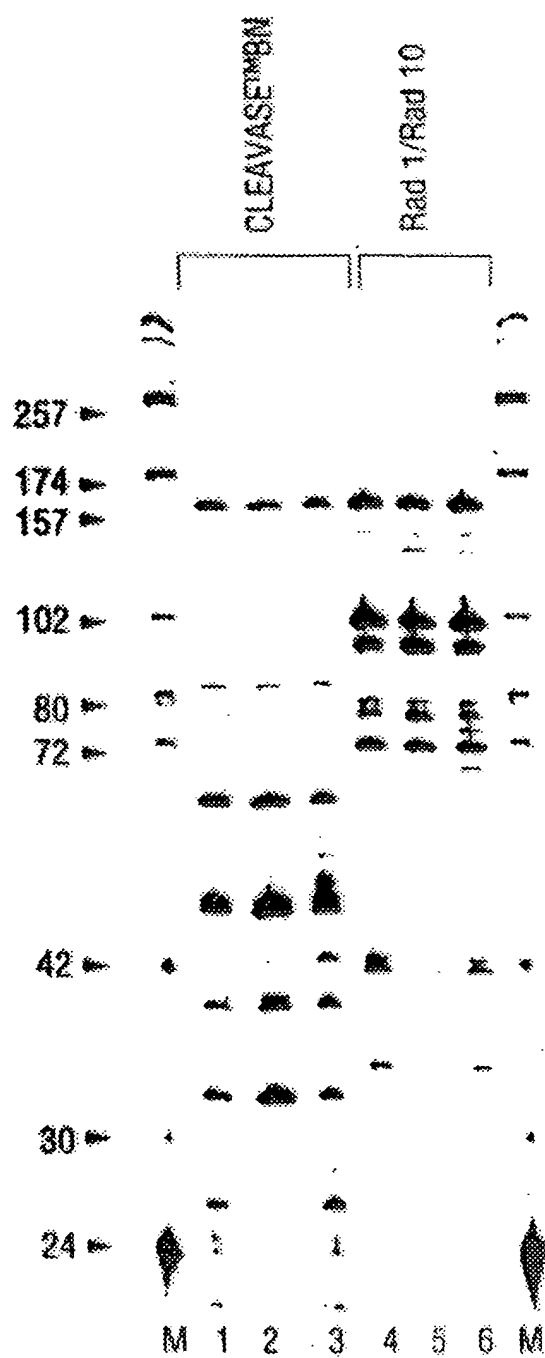


FIG. 72

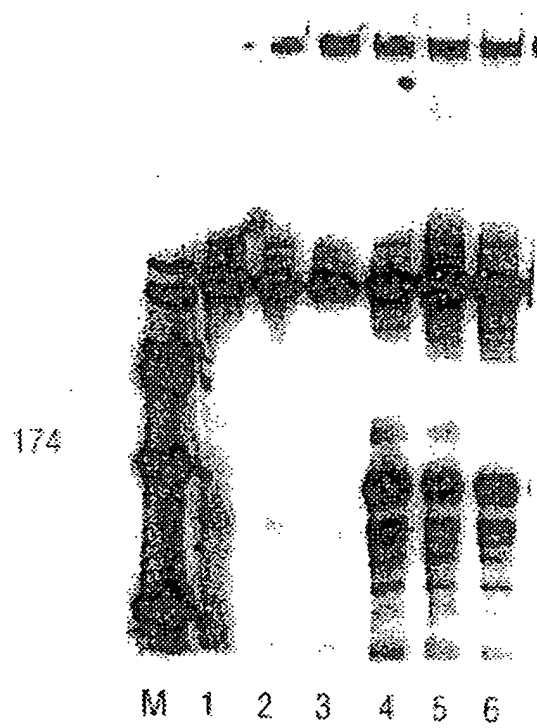


FIG. 73

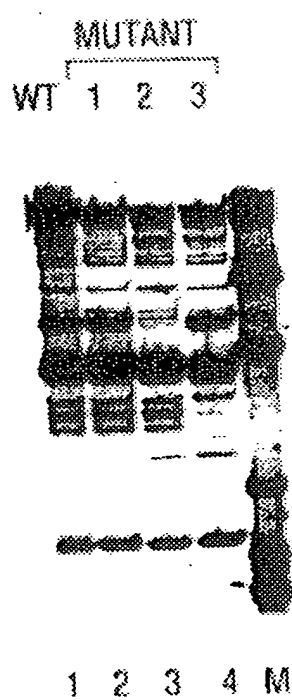


FIG. 74A

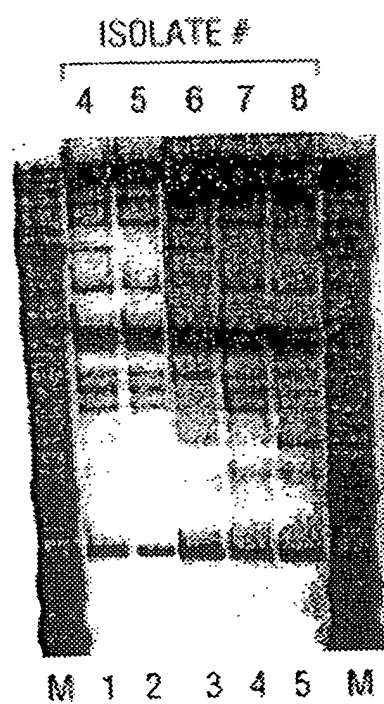


FIG. 74B

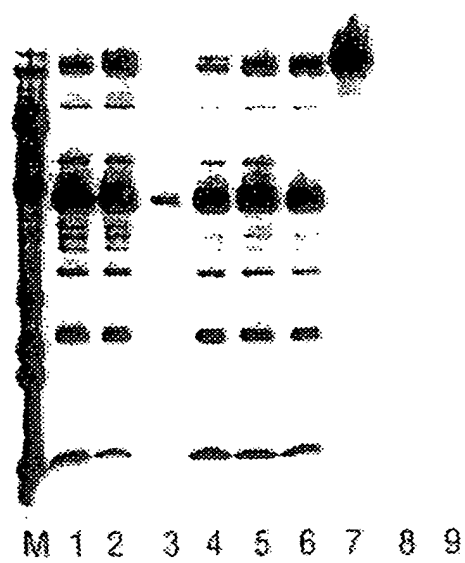


FIG. 75

% OF TOTAL
MUTATIONS

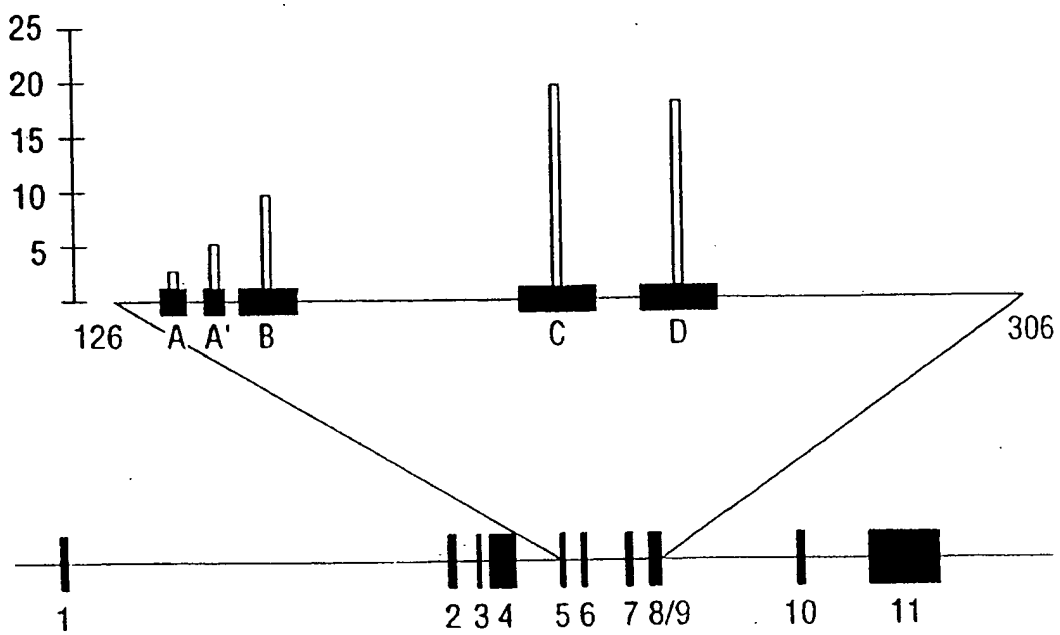


FIG. 76

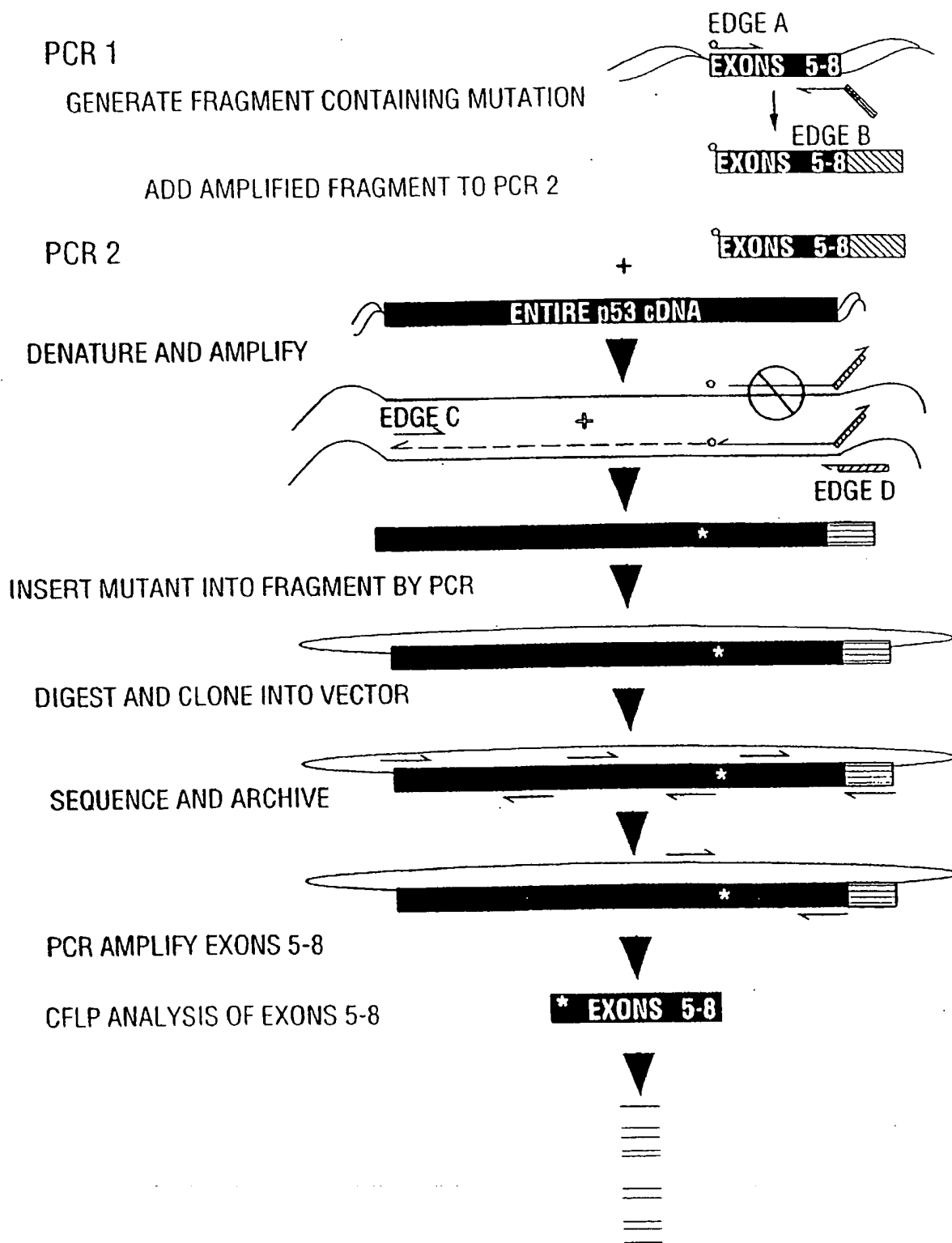


FIG. 77

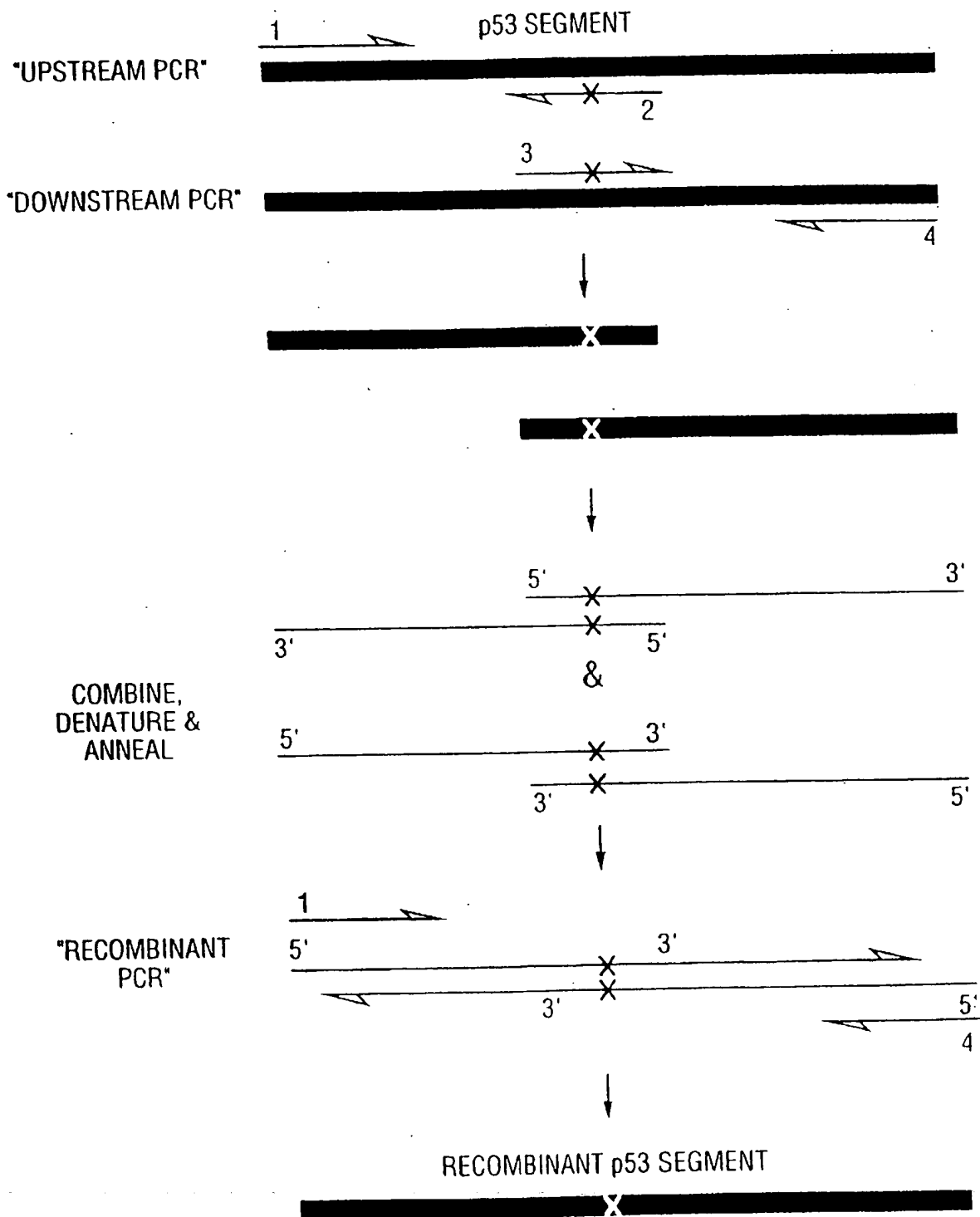


FIG. 78

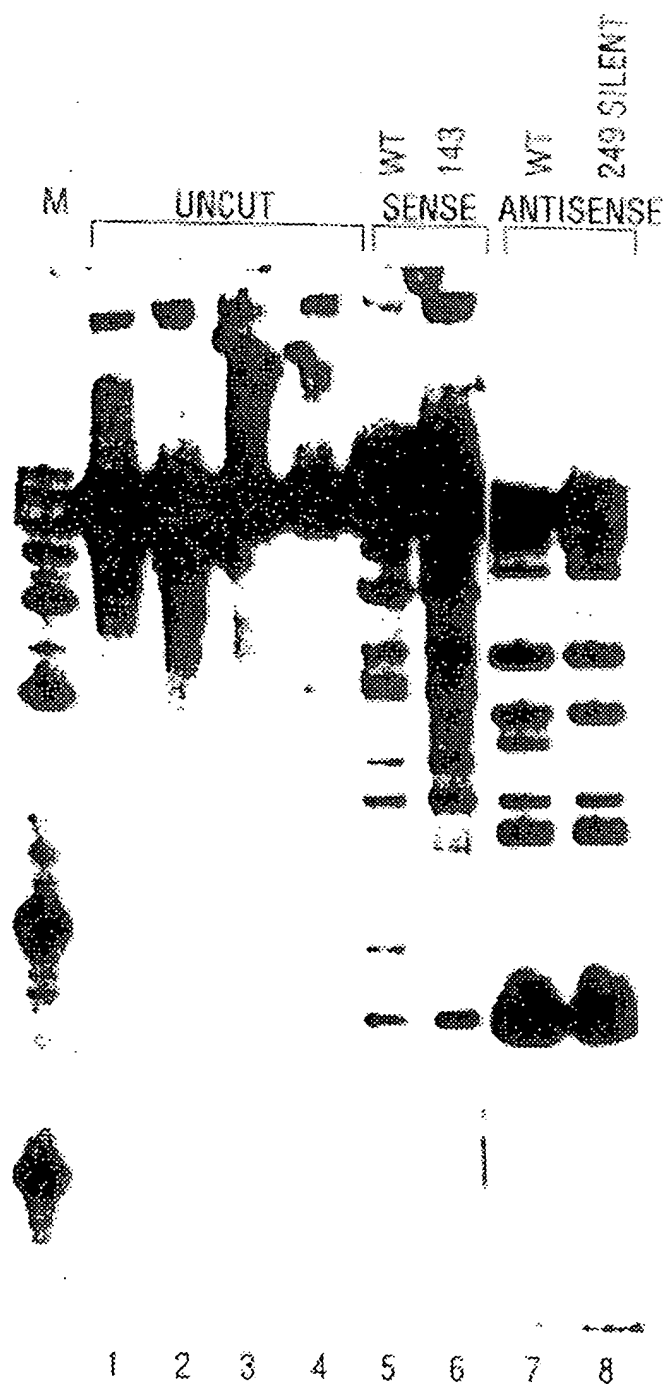


FIG. 79

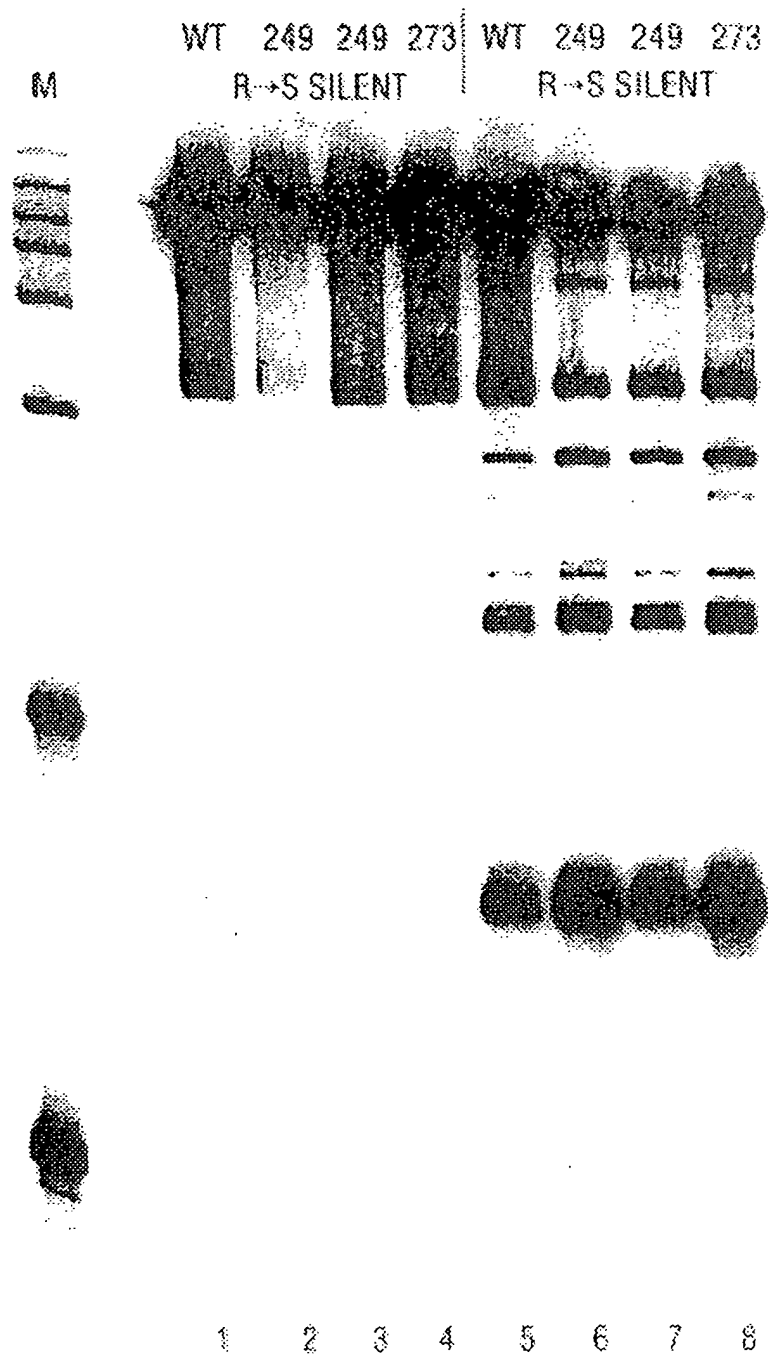


FIG. 80

MIXING PROPORTIONS

		UNCUT	1	1	1	1	0	2	4	9	WILD TYPE
M	WT MUT	0	1	2	9	1	1	1	1	1	MUTANT

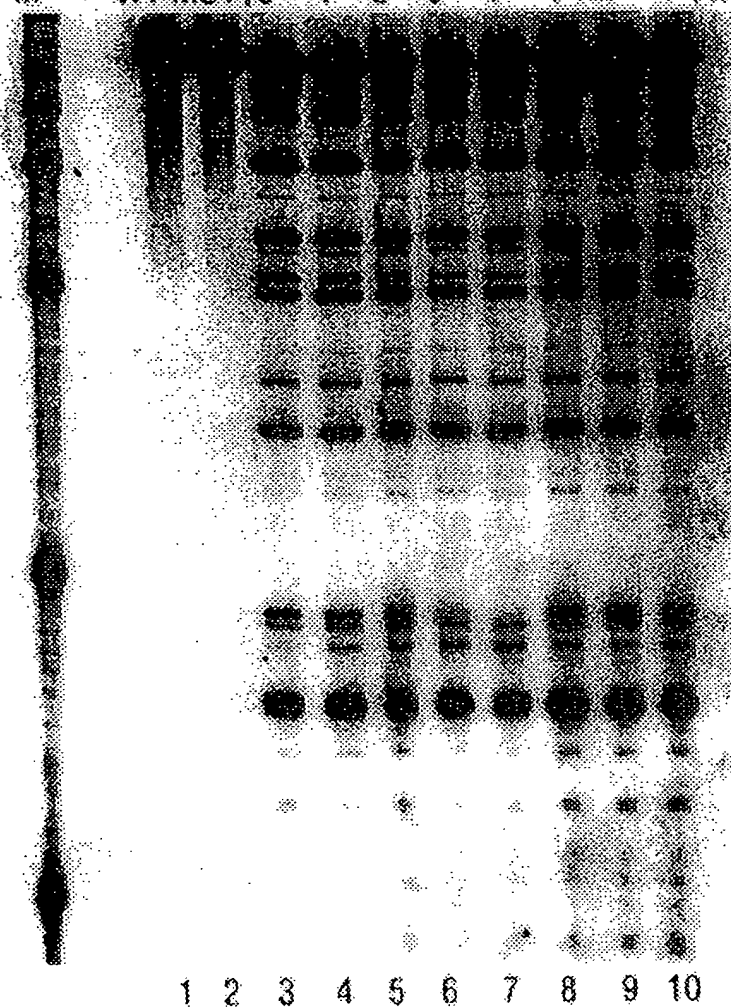


FIG. 81

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTTCAC	GCAGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV3.1	(SEQ ID NO:123)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV4.2	(SEQ ID NO:124)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV6.1	(SEQ ID NO:125)		CTGTCTTTCAC	GCAGAAAGCG	TCTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV7.1	(SEQ ID NO:126)		CTGTCTTTCAC	GCAGAAAGCG	CTAGCCATG	GCGTTAGTAT	GAGTGTCTGTG	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	GGTGGAT <u>GIAA</u>	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT- <u>AAA</u>	
HCV7.1			GGTGAGTACA	CCGGAATCGC	IGGGGIGACC	GGGTCCTTTC	TTGGAG-CAA	

FIG. 82A

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	250
HCV2.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIIGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

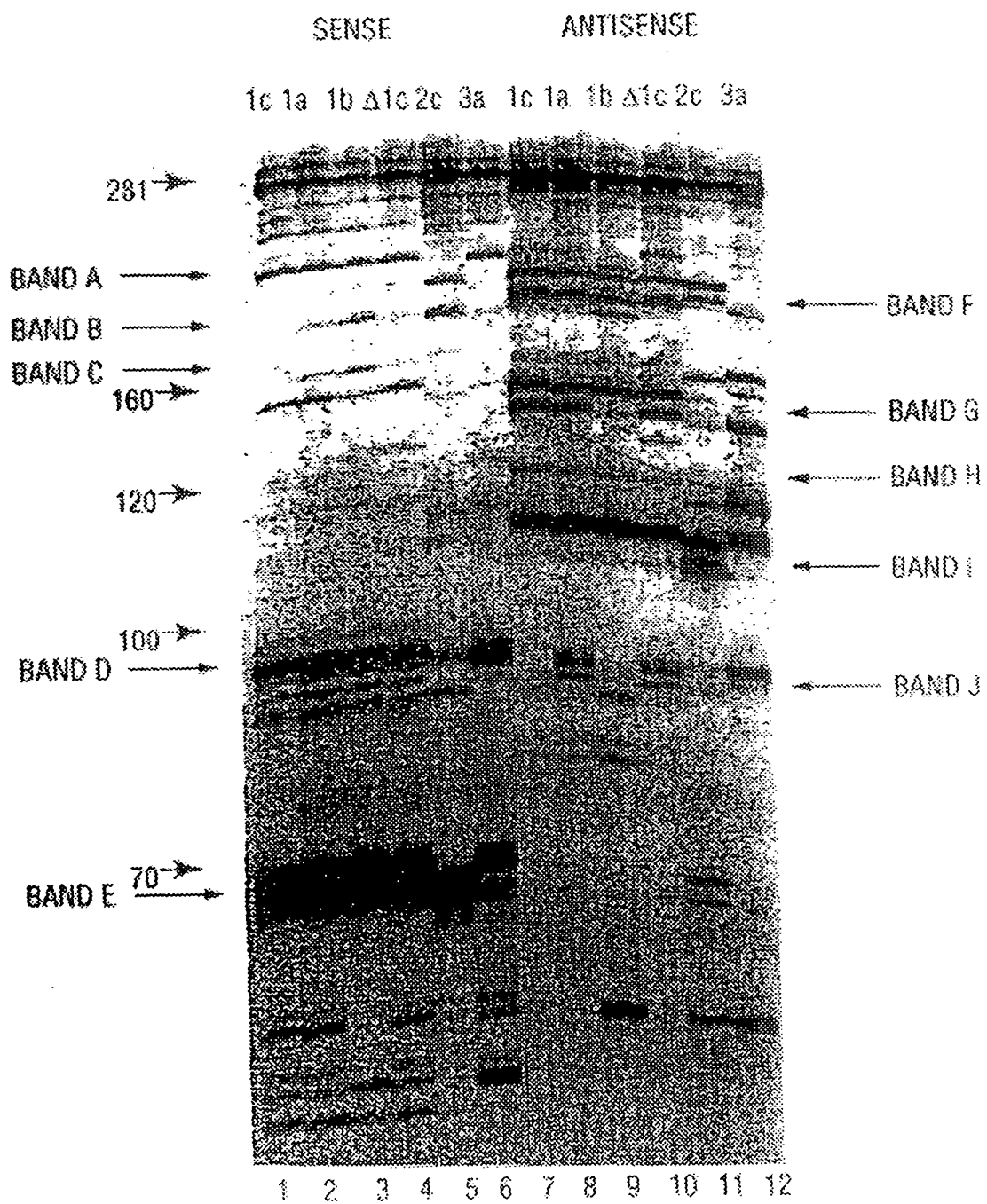


FIG. 83

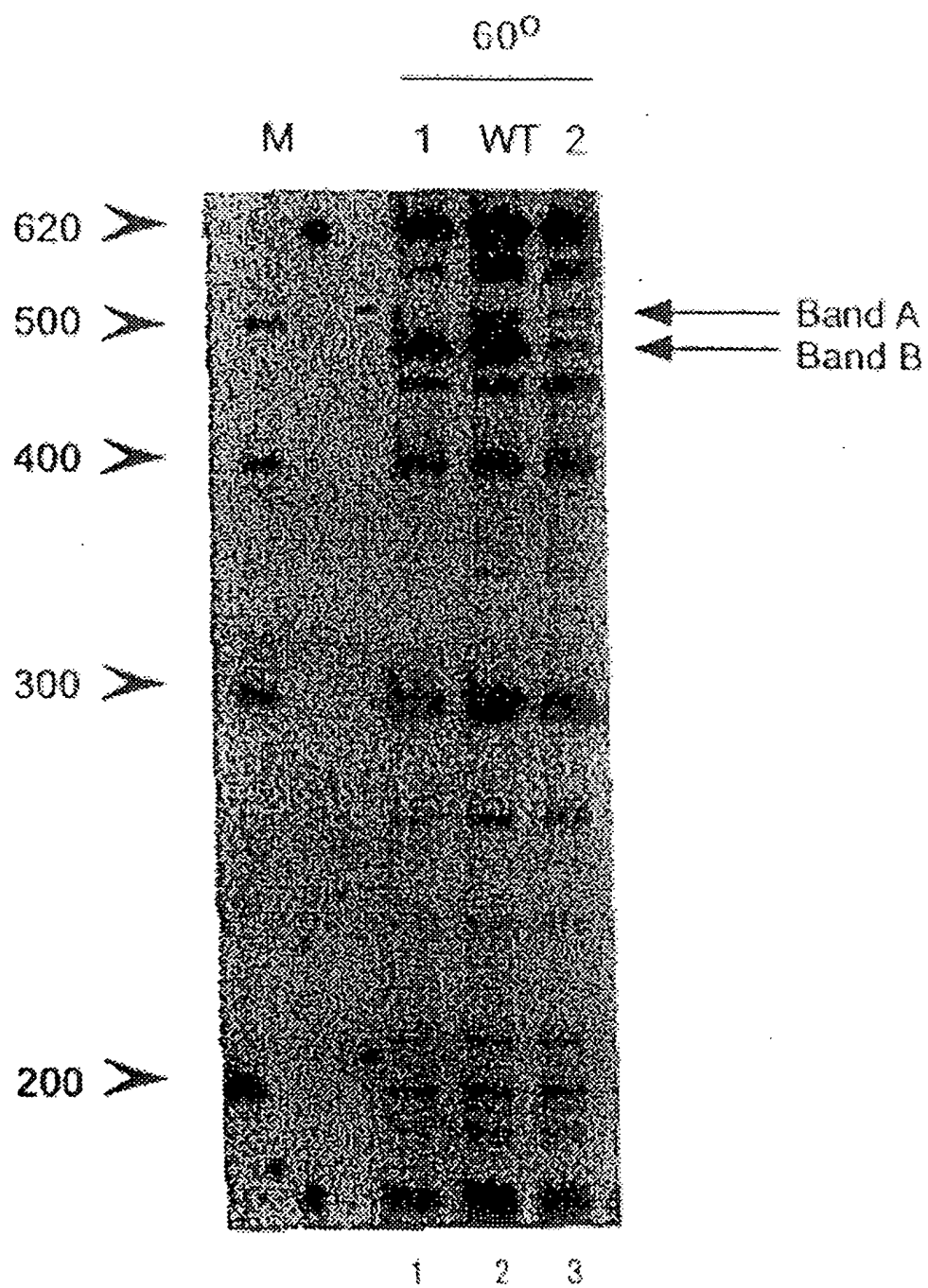


FIG. 84

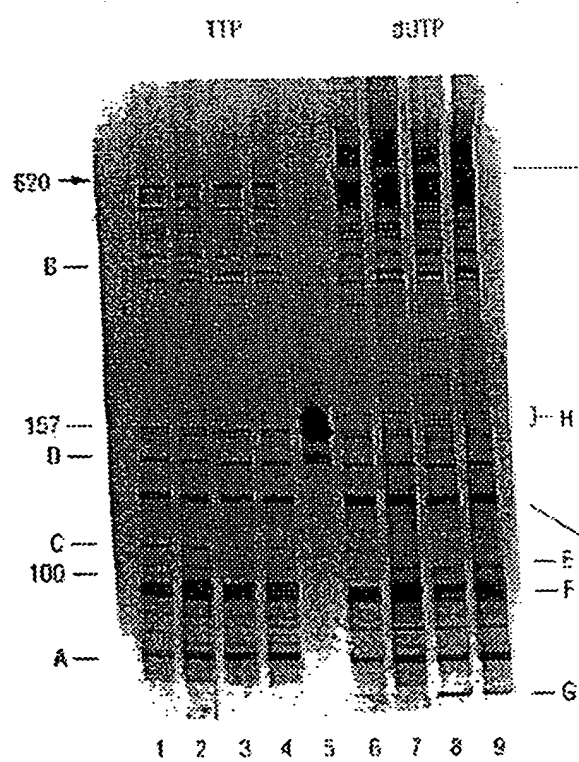


FIG. 85A

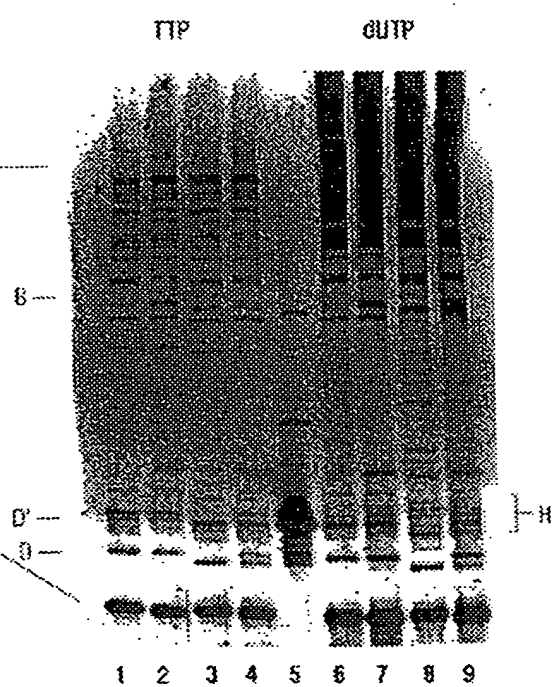


FIG. 85B

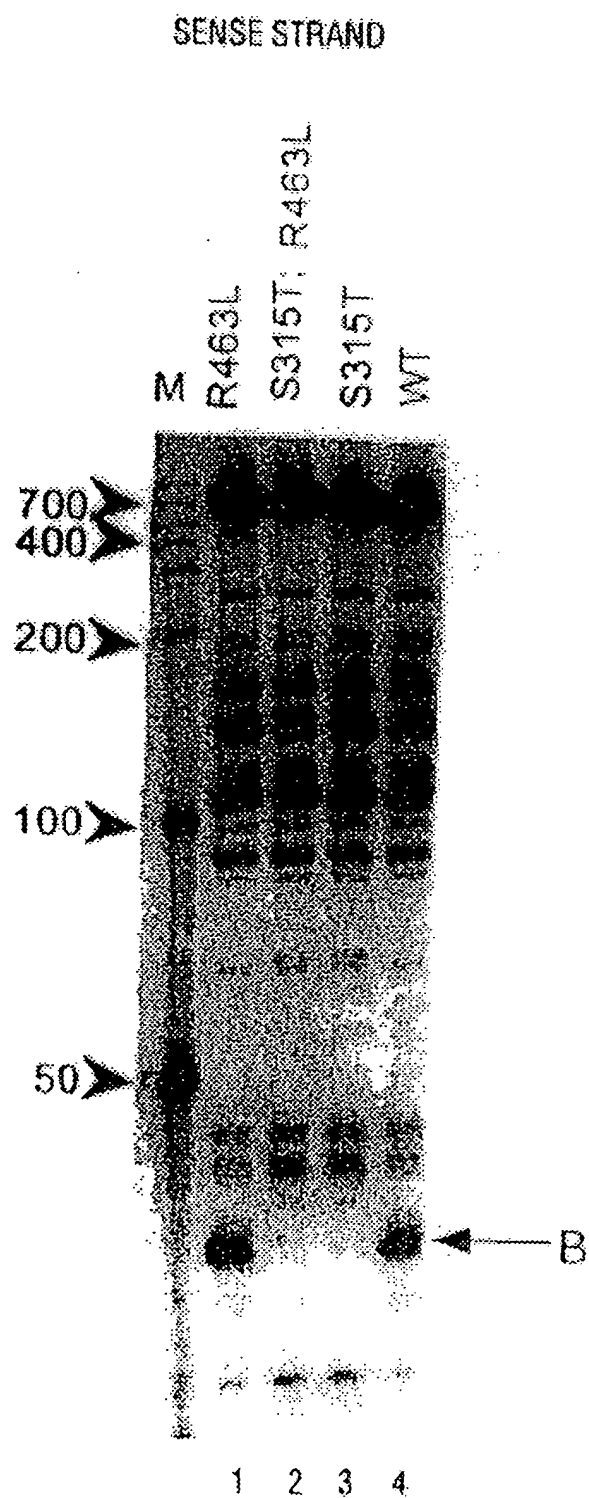


FIG. 86

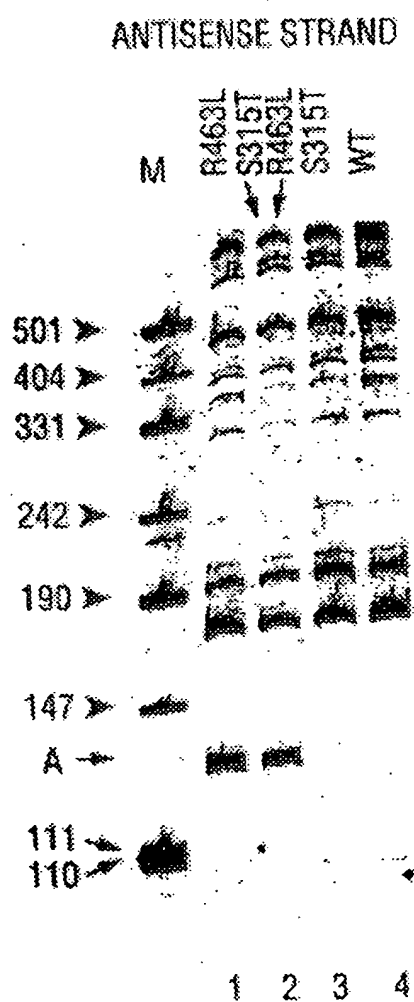


FIG. 87

10	20	30	40	50	60	1638
AGA GTTTGATCCT	GGCTCAG					
AAATTGAAGA	<u>GTTTGATCAT</u>	<u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA	
TTTAACCTTCT	CAAACTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT	
70	80	90	100	110	120	ER10
				GGCGGAC	GGGTGAGTAA	
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGCGGGAC	<u>GGGTGAGTAA</u>	
CAGCTTGCCA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCAT	
130	140	150	160	170	180	
TGTCTGGGAA	ACTGCCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGCCCTCTTG	CCATCGGATG	TGCCCCAGATG	
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGTGGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT	
310	320	330	340	350	360	1659
GGATGACCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG	
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	CCAGGTCTGA	<u>GGATGCCCTC</u>	<u>CGTCGTCACC</u>	
			TGA	GGATGCCCTC	CGTCGTC	

FIG. 88A

370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCGGACTA	CGTCGGTACG	CGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCGC	ATTTGCGGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCCT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

FIG. 88B

AACAGGATTA	790	800	810	820	830	840
TGTCTCTAAT		GATACCCTGG	TAGTCCACGC	CGTAAACGAT	GTCGACTTGG	AGGTTGTGCC
		CTATGGGACC	ATCAGGTGG	GCAATTGCTA	CAGCTGAACC	TCCAACACGG
850		860	870	880	890	900
CTTGAGGCGT		GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCTGGGGAG	TACGGCCGCA
GAACTCCGCA		CCGAAGGCCT	CGATTGGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910		920	930	940	950	960
AGGTTAAAC		TCAAATGAAT	TGACGGGGGC	CCGCACAAGC	GGTGGAGCAT	GTGGTTTAAT
TCCAAATTTG		AGTTTACTTA	ACTGCCCCCG	GGCGTGTTCG	CCACCTCGTA	CACCAAATTA
970		980	990	1000	1010	1020
TCGATGCAAC		GCGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTTT	CAGAGATGAG
AGCTACGTTG		CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCTCTACTC
1030		1040	1050	1060	1070	1080
AATGTGCCCT		CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTCAGCT	CGTGTGTGTA
TTACACGGAA		GCCCCTTGGCA	CTCTGTCCAC	GACGTACCGA	CAGCAGTCGA	GCACAACACT
1090		1100	1110	1120	1130	1140
		GC	AACGAGCGCA	ACCC		
AATGTTGGGT		TAAGTCCCGC	<u>AACGAGCGCA</u>	ACCCTTATCC	TTTGTTGCCA	GCGGTCGGGC
TTACAACCCA		ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG
1150		1160	1170	1180	1190	1200
					ATG	ACGTCAAGTC
					ATG	ACGTCAAGTC
CGGGAAC TCA		AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	<u>ACGTCAAGTC</u>
GCCCTTGAGT		TTCCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCAG

FIG. 88C

1210	1220	1230	1240	1250	1260	
ATCATGGCCC	TTA					SB-3
ATCATGGCCC	TTACGA					SB-4
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAACGG	
<u>TAGTACCGGG</u>	<u>AATGCTGGTC</u>	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTTCGC	
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC	TCGTTGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACCC	TCAGACGTTG	
1330	1340	1350	1360	1370	1380	
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACIIATGCA</u>	1743
				GC	CACCTTATGCA	
1390	1400	1410	1420	1430	1440	
TCCCGGGCCT	TGTACACACC	GCCCCGTACA	CCATGGGAGT	GGGTTGCAAA	AGAAGTAGGT	
<u>AGGGCCCCGA</u>	<u>ACATGTGTGG</u>	CGGGCAGTGT	GGTACCCTCA	CCCAACGTTT	TCTTCATCCA	1743
AGGGCCCCGA	ACATG					
1450	1460	1470	1480	1490	1500	
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	
TCGAATTGGA	AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550		
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....		
GTTCCATTGG	CATCCCCCTG	GACGCCAACCC	TAGTGGAGGA	AT.....		

FIG. 88D

```

1638 (SEQ ID NO:151)      AGAGTTTGATCCTGGCTCAG
E.colirrsE (SEQ ID NO:158)0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGGCTGGCGGCAGGCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159)0 ~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCTGCTAATACATGCA
Stp.aureus (SEQ ID NO:160)0 ..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCCTAATACATGCA

ER10 (SEQ ID NO:152)
E.colirrsE
Cam.jejun5
Stp.aureus
        GCGGGACGGG
60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAGTGGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG

TGAGTAA
114 TGAGTAATGTCTGGGA-AACTGCCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAAACAGTTGGAAACGACTGCTAATA
113 TGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA

175 CCGCATAAC-----GTCCGAAGAC-----CAAAGAGGGGGACCTTCG-GGCCTCTTG
176 CTCTATACTCCTGCTTAACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATAATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT-----CTT----GCTGTCA

221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGTAAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGGATCCGGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
283 CGCTTAAGTGGTCTGAGAGGATGATCAGTCACACTGGAACAGGACACGGTCCAGACTCCTA
291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACAGGACACGGTCCAGACTCCTA
        ACTCCTA
1659 (COMPL)

```

FIG. 89A

E.colirrsE
Cam.jejun5
Stp.aureus
1659(COMPL)

E.colirrsE
Cam.jejun5
Stp.aureus

E.colirrsE
Cam.jejun5
Stp.aureus

345 CCGGAGGCAGCAGTGGGGAATATTGCACAAATGGGCGCAAGCCCTGATGCAGCCATGCCGCCGTG
345 CCGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCCCTGACGCAGCAACGCCGCCGTG
353 CCGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCCTGACGGAGCAACGCCGCCGTG
CGGAGGCAGCAG
407 TATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
407 GAGGATGACACTTTTCGGAGCGTAAACTCTTTCTTTAGGGAAG -----AATT
415 AGTGATGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAAAC
468 ACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCCG
455 C-----TGACGGTACCTAAGGAATAAGCACCCGGCTAACTCCGTGCCAGCAGCCGCCG
476 -TGTCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCCG

FIG. 89B

E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGGGCGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACACTGCTTGGGAAACTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGTCATTGGAAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGGTAGAAATTCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAATTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAAGTGGAATTCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGGATCTGCTGGAACCTCAACTGACGCTAAGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

<i>E.colirrsE</i>	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
<i>Cam. jejuns</i>	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCATTAAGTGTAACCGCCTGGGGAGTACGGTCGC
<i>Stp.aureus</i>	848	GT-TTCCGCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCCTGGGGAGTACGACCCG
<i>E.colirrsE</i>	900	AAGGTTAAAACTCAAATGAATTGACGGGGGCCGACAAAGCGGTGGAGCATGTGGTTTAATT
<i>Cam. jejuns</i>	876	AAGATTAAAACTCAAAGGAATAGACGGGGACCCGCCAAAGCGGTGGAGCATGTGGTTTAATT
<i>Stp.aureus</i>	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCCAAAGCGGTGGAGCATGTGGTTTAATT
<i>E.colirrsE</i>	962	CGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
<i>Cam. jejuns</i>	938	CGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCCTTTTAGAGATAAGAGG
<i>Stp.aureus</i>	971	CGAAGCAACGCGAAGAACCTTACCAAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
<i>E.colirrsE</i>	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGA
<i>Cam. jejuns</i>	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTCAGCTCGTGTGTGA
<i>Stp.aureus</i>	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGATGGTTGTCGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
<i>E.colirrsE</i>	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
<i>Cam. jejuns</i>	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTATTTAGTTGCTAACGGTTCGG-CC
<i>Stp.aureus</i>	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)		ATGACGTC AAGTCATC
SB-4 (SEQ ID NO:154)		ATGACGTC AAGTCATC
E.colirrsE	1142	GGGAAC TCAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152	GGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC
SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTACGA
E.colirrsE	1204	ATGGCCCTTACGACCAGGGCTACACACGTGCTACAAATGGCGCATACAAAGAGAAAGCGACCTC
Cam.jejun5	1183	ATGGCCCTTATGCCCAAGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGGCCCTTATGATTGGGCTACACACGTGCTACAAATGGACAATACAAAGGCGAGCGAAACC
E.colirrsE	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GCGAGGTGGAG-CAATCTATAAAATATGTCCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCCGGGC

FIG. 89E

E.colirrsE	1389	CTTG	TACA	CACG	CCCC	GTCA	CACCAT	GGGAG	TGGG	TGCA	AAAG	AGTAG	GCTTAA	ACCT
Cam.jejun5	1368	CTTG	TACT	CACG	CCCC	GTCA	CACCAT	GGGAG	TGGG	TGCA	AAAG	AGTAG	GCTTAA	ACCT
Stp.aureus	1399	ATTG	TACA	CACG	CCCC	GTCA	CACCAT	GAGAG	TTTG	TAA	CACCCC	GAA	CGCGGTG	GAGTAA
1743(compl)		CTTG	TAC											
E.colirrsE	1451	TCG	GGAG	GGCG	CTTACC	ACTTT	TGTG	ATTCA	TGACT	GGGG	TGA	AGTC	GTAACA	AGGTAAC
Cam.jejun5	1427	AC	---	T-AG	TTAC	CGTCC	CACAG	TGGA	ATCAG	CGACT	GGGG	TGA	AGTC	GTAACA
Stp.aureus	1461	TTT	AGGAG	CTAG	CCCG	TCGA	AGGT	GGGACA	AATGA	TTGG	GGTGA	AGTC	GTAACA	AGGTAAG
E.colirrsE	1512	TAG	GGGA	ACCT	GC	GGT	TGGAT	CAC	CTC	CTTA	---			
Cam.jejun5	1485	TAG	GAGAA	ACCT	GC	GGT	TGGAT	CAC	CTC	CT	----			
Stp.aureus	1523	TAT	CGGA	AGGT	GC	GGCT	GGAT	CAC	CTC	CT	TTCT			

FIG. 89F

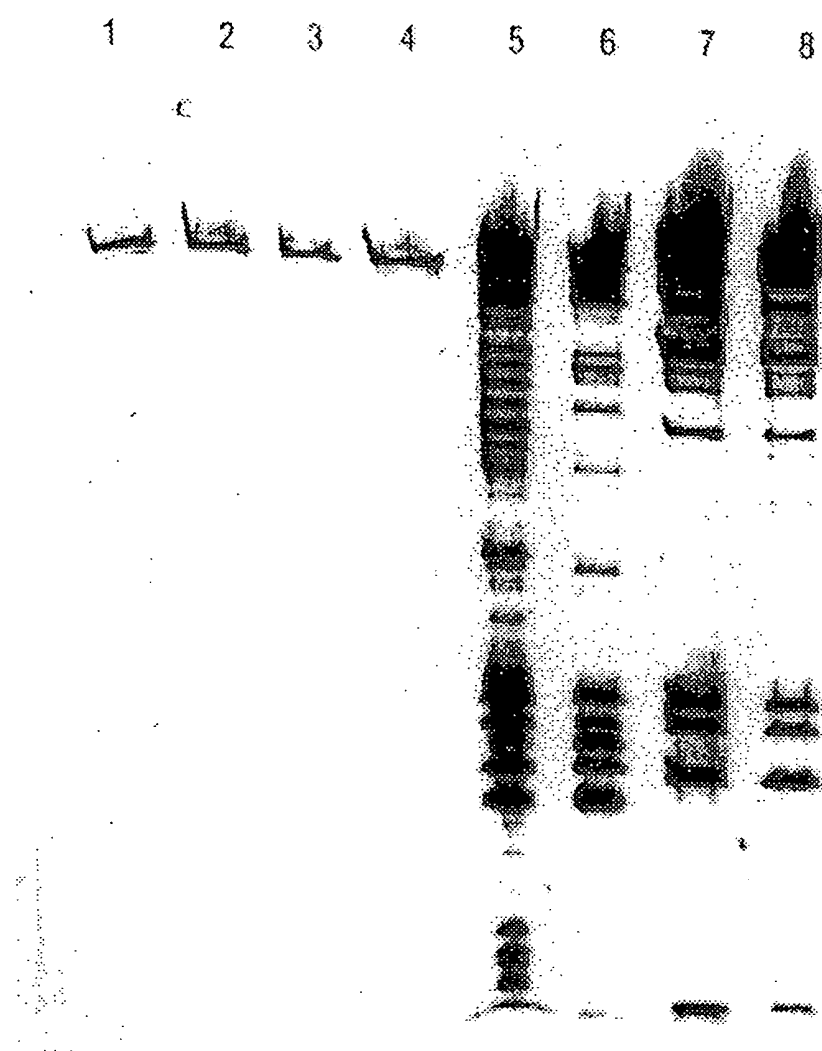


FIG. 90

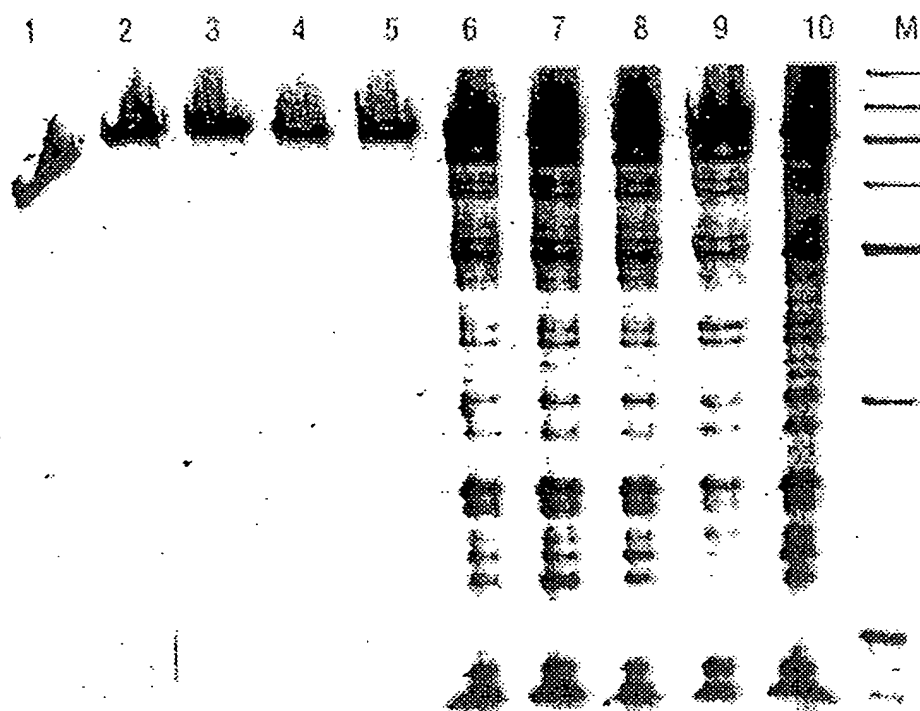


FIG. 91A

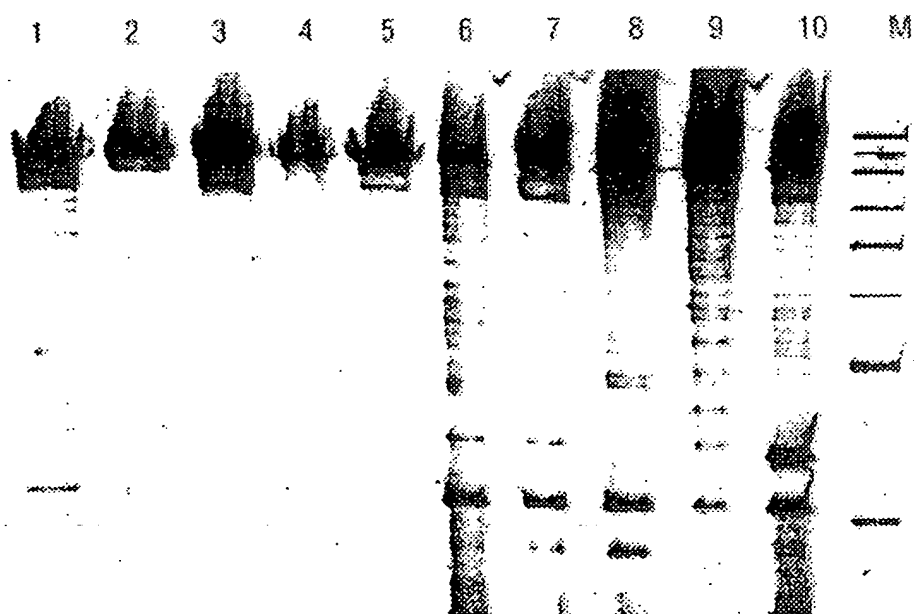


FIG. 91B

1 2 3

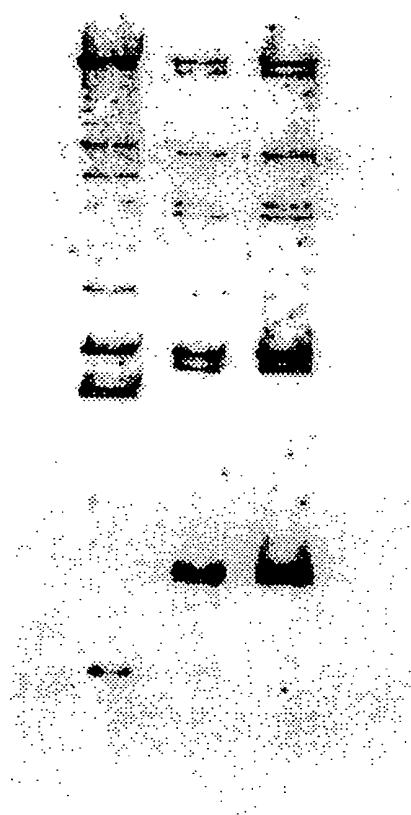


FIG. 92

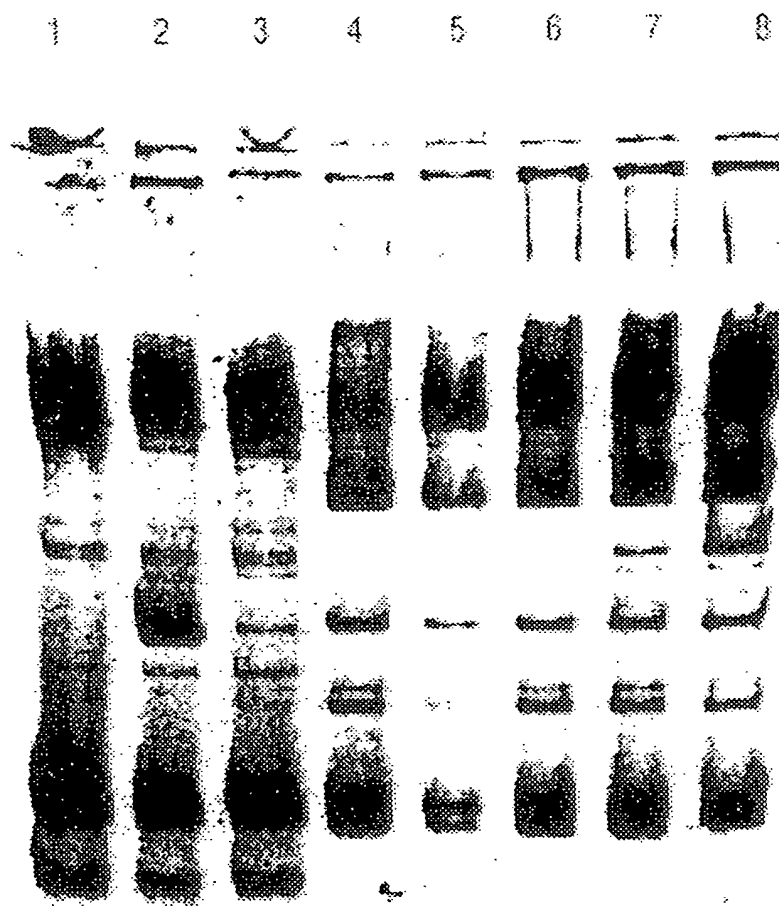


FIG. 93

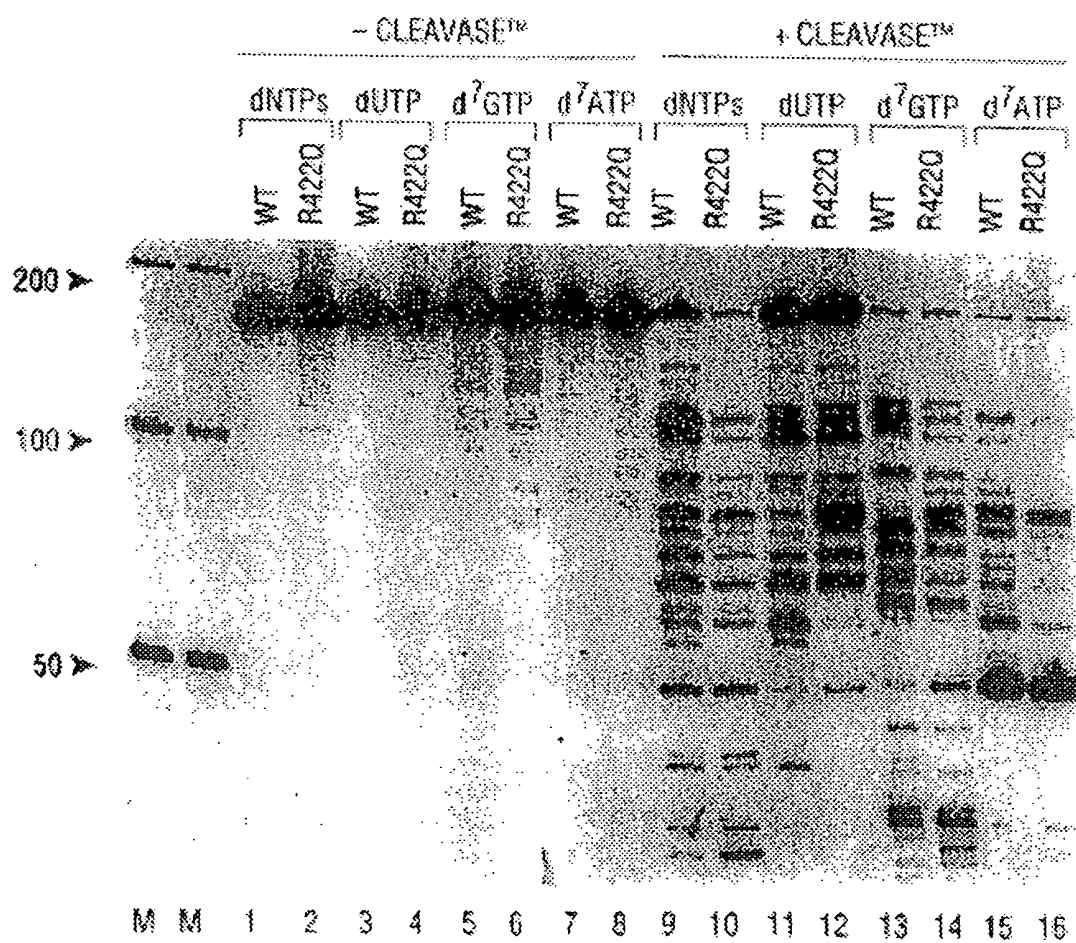


FIG. 94